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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:41:34 ; Search time 75 Seconds
(without alignments)
950.521 Million cell updates/sec

Title: US-09-888-035A-2

Perfect score: 2722

Sequence: 1 MGMEVAARALGALYTTSDYA.....GRGFVFPSPGTEQSHGGR 535

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_101002.*

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- 2: /SID32/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID32/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID32/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 20: /SID32/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID32/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID32/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2722	100.0	535	21	AA11832
2	2105.5	77.4	555	21	AA11832
3	2103.5	77.3	540	22	AA12786
4	2095.5	77.0	553	22	AA12786
5	2055.5	75.5	542	22	AA12786
6	2023.5	74.3	538	20	AA12786
7	1966	72.2	555	22	AA12786
8	1852.5	68.1	547	20	AA12786
9	1799.5	66.1	571	22	AA12786
10	1550.5	57.0	556	23	AA12786

11	1529	56.2	529	20	AA12786
12	618	22.7	671	23	AA12786
13	600.5	22.1	608	21	AA12786
14	595.5	21.9	649	22	AA12786
15	565.5	20.8	673	23	AA12786
16	565	20.8	727	22	AA12786
17	552	20.3	569	20	AA12786
18	541.5	19.9	509	22	AA12786
19	541.5	19.9	509	23	AA12786
20	541.5	19.9	526	22	AA12786
21	539	19.8	631	23	AA12786
22	533	19.6	633	20	AA12786
23	481	17.7	816	14	AA12786
24	479.5	17.6	834	18	AA12786
25	475.5	17.5	518	22	AA12786
26	448	16.5	707	23	AA12786
27	448	16.5	717	23	AA12786
28	439	16.1	325	20	AA12786
29	425.5	15.6	605	22	AA12786
30	416.5	15.3	664	22	AA12786
31	369.5	13.6	273	22	AA12786
32	362	13.3	275	22	AA12786
33	350	12.9	315	22	AA12786
34	312	11.5	531	23	AA12786
35	303.5	11.1	359	22	AA12786
36	292.5	10.7	339	22	AA12786
37	292.5	10.7	339	22	AA12786
38	292.5	10.7	339	23	AA12786
39	292.5	10.7	339	23	AA12786
40	288	10.6	990	22	AA12786
41	285.5	10.5	1146	23	AA12786
42	284	10.4	707	22	AA12786
43	284	10.4	707	22	AA12786
44	273	10.0	232	20	AA12786
45	252.5	9.3	511	22	AA12786

ALIGNMENTS

RESULT 1

AA11832

ID AA11832 standard; Protein: 535 AA.

XX AA11832;

XX 07-NOV-2000 (first entry)

XX Rice Na+/H+ antiporter, OsNHX1.

XX OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.

OS Oryza sativa.

PN WO200037644-A1.

PD 29-JUN-2000.

PF 22-DEC-1999; 99WO-JP07224.

PR 22-DEC-1998; 98JP-0365604.

XX (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.

XX Fukuda A, Tanaka Y;

XX WPI; 2000-442672/38.

XX N-PSDB; AAA61876.

XX DNA encoding a sodium ion and proton counter-transporter protein of

XX rice origin for production of salt tolerant rice transformants

XX

Physcomitrella pat

PS Claim 1a; Fig 1; 43pp; Japanese.
 XX This sequence represents a novel rice Na⁺/H⁺ antiporter
 CC (countertransporter), OSHX1. The invention relates to OSHX1 and
 CC nucleic acids which encode it; vectors, host cells and transgenic plants
 CC containing OSHX1 nucleic acids; recombinant expression of OSHX1; and
 CC antibodies which recognise OSHX1. OSHX1 nucleic acids are useful in the
 CC production of salt tolerant transgenic plants.
 XX
 SQ Sequence 535 AA;
 Query Match 100.0%; Score 2722; DB 21; Length 535;
 Best Local Similarity 100.0%; Pred. No. 8.4e-271;
 Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGMEVAAARLGALYTTSDYASVSVINLFVALLCACIVLGHLEENRWVNESITALLIGLC 60
 DB 1 MGMEVAAARLGALYTTSDYASVSVINLFVALLCACIVLGHLEENRWVNESITALLIGLC 60
 QY 61 TGVVILLMTKGSSHLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGT 120
 DB 61 TGVVILLMTKGSSHLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGT 120
 QY 121 MISFETISIAAIAIFSRMNIPTLDVGDFLAIGAIFSDTSVCTLOVLDQDETFPFLYSLVF 180
 DB 121 MISFETISIAAIAIFSRMNIPTLDVGDFLAIGAIFSDTSVCTLOVLDQDETFPFLYSLVF 180
 QY 181 GGGVNDATSI VLFNALQNFDLVHIDAAVVLKFLGNFFYFLFSSTFLGVFAGLLSAYIITK 240
 DB 181 GGGVNDATSI VLFNALQNFDLVHIDAAVVLKFLGNFFYFLFSSTFLGVFAGLLSAYIITK 240
 QY 241 KLYIGRHSITREVALMLMAYLSYMLAELLDSGLTVFFCGIVMSHYTNHNVTESSRVT 300
 DB 241 KLYIGRHSITREVALMLMAYLSYMLAELLDSGLTVFFCGIVMSHYTNHNVTESSRVT 300
 QY 301 TKHAFATLSFAETFLFYVGMNDALDIEKWEFASDRPKSGISGILLGLVLIGRAAFV 360
 DB 301 TKHAFATLSFAETFLFYVGMNDALDIEKWEFASDRPKSGISGILLGLVLIGRAAFV 360
 QY 361 PLSFSLNLTAKAPNEKITRWQOVVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMIT 420
 DB 361 PLSFSLNLTAKAPNEKITRWQOVVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMIT 420
 QY 421 STITVVFSTVFMGMTKPLIRLLPASGHPVTSEPPSPKSLHSPPLTSMOGSDLESTN 480
 DB 421 STITVVFSTVFMGMTKPLIRLLPASGHPVTSEPPSPKSLHSPPLTSMOGSDLESTN 480
 QY 481 IVRPSSRLMLTKPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQSHGGR 535
 DB 481 IVRPSSRLMLTKPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQSHGGR 535
 RESULT 2
 AAB12786
 ID AAB12786 standard; Protein; 555 AA.
 XX
 AC AAB12786;
 XX
 DT 23-NOV-2000 (first entry)
 XX
 DE Atliplex gmelini Na⁺ and H⁺ antiporter protein.
 XX
 KW Atliplex gmelini; Na⁺ plus and H⁺ plus antiporter protein;
 XX Na⁺ and H⁺ antiporter protein; transformed plant; high salt tolerance.
 XX
 OS Atliplex gmelini.
 XX
 PN JP2000157287-A.
 XX
 PD 13-JUN-2000.
 XX
 PF 16-SEP-1999; 99JP-0261606.
 XX

PR 24-SEP-1998; 98JP-0269504.
 XX (SHOK-) SHOKUBUTSU KOGAKU KK.
 XX
 DR WPI; 2000-468209/41.
 DR N-PSDB; AAA72926.
 XX
 PT An Na⁺ and H⁺ plus antiporter protein and a gene encoding it -
 PS Disclosure; Page 10-12; 16pp; Japanese.
 XX
 CC The present sequence represents an Na⁺ and H⁺ antiporter protein
 CC isolated from Atliplex gmelini. The Na⁺ and H⁺ antiporter protein and
 CC gene encoding it are useful for the preparation of transformed plants
 CC with high salt tolerance, e.g. for growth in arid land.
 XX
 SQ Sequence 555 AA;
 Query Match 77.4%; Score 2105.5; DB 21; Length 555;
 Best Local Similarity 76.1%; Pred. No. 2.2e-207;
 Matches 410; Conservative 53; Mismatches 61; Indels 15; Gaps 4;
 QY 7 AARLALYTTSDYASVSVINLFVALLCACIVLGHLEENRWVNESITALLIGLGTGWL 66
 DB 10 SGKMDAL-TTSDHASVSMNLFVALLCGCIVIGHLEENRWVNESITALLIGLGTGWL 68
 QY 67 LMTKCKSSHLFVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGTMSFT 126
 DB 69 LISGCKSSHLVSEDLFFIYLLPPIIFNAGFOVKKQFFRNPMITLFGAVGTLSFT 128
 QY 127 ISIAAIAIFSRMNIPTLDVGDFLAIGAIFSDTSVCTLOVLDQDETFPFLYSLVFGGVN 186
 DB 129 ISLGALSIFKLDIGTLEADYLAIGAIFAATDSVCTLOVLDQDETFPFLYSLVFGGVN 188
 QY 187 DATSIVLFNALQNFDLVHIDAAVVLKFLGNFFYFLFSSTFLGVFAGLLSAYIITKLYIGR 246
 DB 189 DATSVLFNALQSFDTLRIDHRIALQFMGNFLYLFIASTILGAFGLLSAYIITKLYIGR 248
 QY 247 HSTDREVALMLMAYLSYMLAELLDSGLTVFFCGIVMSHYTNHNVTESSRVTKHAF 306
 DB 249 HSTDREVALMLMAYLSYMLAELLDSGLTVFFCGIVMSHYTNHNVTESSRVTKHAF 308
 QY 307 TLSFTAETFLFYVGMNDALDIEKWEFASDRPKSGISGILLGLVLIGRAAFVFLSFLS 366
 DB 309 TLSFVAEFLFYVGMNDALDIEKWEFASDRPKSGISGILLGLVMGAAAFVFLSFLS 368
 QY 367 NLTKKAPNEKITRWQOVVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMITSTITVV 426
 DB 369 NFAKSQSEKVTFNQOVIWAGLMRGAVSIALAYNKFTRSQHTQLHGNAMITSTISVV 428
 QY 427 LFTSMVFMGMTKPLIRLLPASGH----PVTSEPPSPKSLHSPPLTSMOGSDL----- 475
 DB 429 LFTSMVFMGLLTKPLIMFLPQPKFTSCSTVSDVSPKSYSLPGLLEGNDQYEDVGVNGNH 488
 QY 476 ESTT---NIVRPSSRLMLTKPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQS 531
 DB 489 EDTTEPTVIRPSSRLMLNAPHTVHYVWRKFDALMRPMFGGRGVFPFSPGSPTEQS 547
 RESULT 3
 AAB73252
 ID AAB73252 standard; Protein; 540 AA.
 XX
 AC AAB73252;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Protein regulating the pH of vacuoles.
 XX
 KW Vacuole pH regulation; flower colour.
 XX
 OS Petunia hybrida.
 XX

PN WO200114560-A1.
 XX 01-MAR-2001.
 PD 24-AUG-2000; 2000WO-JP05722.
 XX 24-AUG-1999; 99JP-0236800.
 PF (SUNR) SUNTORY LTD.
 XX Iida S, Tanaka S, Inagaki Y;
 PI WPI: 2001-191648/19.
 DR N-PSDB; AAF75764.
 XX Morning glory-originated gene encoding a protein with pH regulation
 PT activity in vacuoles, useful in controlling flower color to give new
 PT breeds of colorful plants for cut flowers, particularly applicable in
 PT horticulture -
 XX Example 7; Page 42-45; 68pp; Japanese.
 PS The present sequence is a protein, which has vacuolar pH regulatory
 CC activities. The protein enables flower colour to be controlled via
 CC regulation of the vacuolar pH, colours can range from blue to red in
 CC colour spectrum. The protein is useful in controlling flower colour to
 CC give new breeds of colourful plants for cut flowers, particularly
 CC applicable in horticulture.
 XX Sequence 540 AA;
 SQ Query Match 77.3%; Score 2103.5; DB 22; Length 540;
 Best Local Similarity 77.4%; Pred. No. 3.4e-207;
 Matches 404; Conservative 53; Mismatches 62; Indels 3; Gaps 1;
 QY 15 TTSYASVSVINLFAVALLCIVGLHLEENRWYNESITALIIGLCTGVILLMTKGSS 74
 DB 16 STSDHQSVSVINLFAVALLCIVGLHLEENRWYNESITALVIGSGTGIVILLISGGKNS 75
 QY 75 HLFVSEDLFFIYLLPPIIFNAGFQVKKQFFRNPMFTITLFGAVGTMISFETISAAIAI 134
 DB 76 HILVSEDLFFIYLLPPIIFNAGFQVKKQFFRNPMFTITLFGAVGTMISFETISAAIAI 135
 QY 135 FSRMNIIGLDVGDFAIGAIFATSQVCTLOVLNDETPFYLSLVFGGVNDATSVILF 194
 DB 136 FRKMNIIGLEIGDYLGAIGAIFATSQVCTLOVLNDETPFYLSLVFGGVNDATSVILF 195
 QY 195 NALQNFDLVHDAAVVLLKFLNGFFYFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDEVA 254
 DB 196 NALQNFDLSHIDTGKAMELVGNFLYLFASSTALGVAAGLLSAYIIKKLYIGRHSTDEVA 255
 QY 255 LMMLMAYLSYMLAELDLGLTIVFFCGIVMSHYTHWNTVTSRVTTHKFAFATLSFAET 314
 DB 256 IMILMAYLSYMLAELFYLSAILTVFFGIVMSHYTHWNTVTSRVTTHKFAFATLSFAEI 315
 QY 315 FLFYVGMADALDIEKWEFASDRPGKSGISSTILLGLVLIIGRAAFVFPFLSFLSNLTKKAPN 374
 DB 316 FLFYVGMADALDIEKWFVSDSPGISVQVSSILLGLVLGVRAAFVFPFLSFLSNLTKKYPE 375
 QY 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTSRGHTQLHGNAIMTITITVVLFTWVFG 434
 DB 376 AKISFQOQVTIWWAGLMRGAVSMALAYNQFTRGHTQLRANAIMTITITVVLFTWVFG 435
 QY 435 MMTKPLIRILLPASGH--PVTSSESPKSLSPHLLTSNQGSDLESTNIVRPSLRMLL 491
 DB 436 LMTKPLIRILLPSHKLRSMTSEPTPKSFIVPLDSTQDSEADLERVPRPHSLRMLL 495
 QY 492 TKPHTHYVYWRKFDALMRPFGGRGVFPSPGSPTEOSHG 533
 DB 496 STPSHTHYVYWRKFDNAEMRPVFGGRGVFPFAPGSPTEDPVG 537
 RESULT 4

AAB73253
 ID AAB73253 standard; Protein; 553 AA.
 XX AAB73253;
 AC 14-MAY-2001 (first entry)
 DT Protein regulating the pH of vacuoles.
 DE Vacuole pH regulation; flower colour.
 XX Nierembergia hybrida.
 OS WO200114560-A1.
 PN 01-MAR-2001.
 PD 24-AUG-2000; 2000WO-JP05722.
 PF 24-AUG-1999; 99JP-0236800.
 PR (SUNR) SUNTORY LTD.
 PA Iida S, Tanaka S, Inagaki Y;
 XX WPI: 2001-191648/19.
 DR N-PSDB; AAF75765.
 XX Morning glory-originated gene encoding a protein with pH regulation
 PT activity in vacuoles, useful in controlling flower color to give new
 PT breeds of colorful plants for cut flowers, particularly applicable in
 PT horticulture -
 XX Example 7; Page 50-52; 68pp; Japanese.
 PS The present sequence is a protein, which has vacuolar pH regulatory
 CC activities. The protein enables flower colour to be controlled via
 CC regulation of the vacuolar pH, colours can range from blue to red in
 CC colour spectrum. The protein is useful in controlling flower colour to
 CC give new breeds of colourful plants for cut flowers, particularly
 CC applicable in horticulture.
 XX Sequence 553 AA;
 SQ Query Match 77.0%; Score 2095.5; DB 22; Length 553;
 Best Local Similarity 77.8%; Pred. No. 2.3e-206;
 Matches 403; Conservative 49; Mismatches 63; Indels 3; Gaps 1;
 QY 15 TTSYASVSVINLFAVALLCIVGLHLEENRWYNESITALIIGLCTGVILLMTKGSS 74
 DB 16 TTSYASVSVINLFAVALLCIVGLHLEENRWYNESITALVIGSGTGIVILLISGGKNS 75
 QY 75 HLFVSEDLFFIYLLPPIIFNAGFQVKKQFFRNPMFTITLFGAVGTMISFETISAAIAI 134
 DB 76 HILVSEDLFFIYLLPPIIFNAGFQVKKQFFRNPMFTITLFGAVGTMISFETISAAIAI 135
 QY 135 FSRMNIIGLDVGDFAIGAIFATSQVCTLOVLNDETPFYLSLVFGGVNDATSVILF 194
 DB 136 FRKMNIIGLEIGDYLGAIGAIFATSQVCTLOVLNDETPFYLSLVFGGVNDATSVILF 195
 QY 195 NALQNFDLVHDAAVVLLKFLNGFFYFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDEVA 254
 DB 196 NALQNFDLSHIDTGKAMELVGNFLYLFASSTALGVAAGLLSAYIIKKLYIGRHSTDEVA 255
 QY 255 LMMLMAYLSYMLAELDLGLTIVFFCGIVMSHYTHWNTVTSRVTTHKFAFATLSFAET 314
 DB 256 IMILMAYLSYMLAELFYLSAILTVFFGIVMSHYTHWNTVTSRVTTHKFAFATLSFAEI 315
 QY 315 FLFYVGMADALDIEKWEFASDRPGKSGISSTILLGLVLIIGRAAFVFPFLSFLSNLTKKAPN 374
 DB 316 FLFYVGMADALDIEKWFVSDSPGISVQVSSILLGLVLGVRAAFVFPFLSFLSNLTKKYPE 375
 QY 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTSRGHTQLHGNAIMTITITVVLFTWVFG 434

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Db 376 KRISNQVTTIWWAGLMRGAVSMALAYNOFTRGGHTQLRANAIMTSTITVVLFTSVVFG 435
QY 435 MMTKPLIRILLPASGH---PVTSEPPSKSLHSPLLTSMQGSDELESTTNIVRPSSLRMLL 491
Db 436 LMTKPLILLLLPSOKHLIRMSSEPMTPKSFIVPLDSTQDSEADLGRHVPSPHSLRMLL 495
QY 492 TKPTVTYVYWRKFDALMRPFGRGVPFPGSPTE 529
Db 496 STPSHTVYVYWRKFDNAFMFPVFGGRGVPFPGSPTE 533

RESULT 5
AAB73251
ID AAB73251 standard; Protein: 542 AA.
XX
AC AAB73251;
XX
DT 14-MAY-2001 (first entry)
XX
DE Protein regulating the pH of vacuoles.
XX
KW Vacuole pH regulation; morning glory; flower colour.
XX
OS Ipomoea nil.
XX
PN WO200114560-A1.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP05722.
XX
PR 24-AUG-1999; 99JP-0236800.
XX
PA (SUNR ) SUNTORY LTD.
XX
PI Iida S, Tanaka S, Inagaki Y;
XX
DR WPI: 2001-191648/19.
DR N-PSDB: AAF75752.
XX
PT Morning glory-originated gene encoding a protein with pH regulation
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture
XX
PS Claim 2; Page 30-33; 68pp; Japanese.
XX
CC The present sequence is a protein from Morning Glory, which has vacuolar
CC pH regulatory activities. The protein enables flower colour to be
CC controlled via regulation of the vacuolar pH, colours can range from blue
CC to red in colour spectrum. The protein is useful in controlling flower
CC colour to give new breeds of colourful plants for cut flowers,
CC particularly applicable in horticulture.
XX
SQ Sequence 542 AA;

Query Match 75.5%; Score 2055.5; DB 22; Length 542;
Best Local Similarity 76.4%; Pred. No. 2.9e-202;
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;

QY 16 TSDYASVSVINLFAVLLCAGTIVGLHLEENRWNESTALIIIGLCTGVILLMTYKGSKH 75
Db 16 TSDHASVSMNLFVALLCAGTIVGLHLEENRWNESTALIIIGLCTGVILLMTYKGSKH 75
QY 76 LFVSEDLFFIYLLPPIIFNAGFVKKKOPERNEMTITLFGAVGTMTSFFTISTATAIF 135
Db 76 LFVSEDLFFIYLLPPIIFNAGFVKKKOPERNEMTITLFGAVGTMTSFFTISTATAIF 135
QY 136 SRMNIPTLDVDFIAIGAIFSAITSDSVCTLOVLNODETPFYLSLVFGGVNDATSVLNF 195
Db 136 KHLIDFLDFDGYLAIGAIFAATSDSVCTLOVLSQDETPLYLSLVFGGVNDATSVLNF 195

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QY 196 ALQNFEDLVHDAAVVLKFLGNFFYFLSLSTFLGVFAGLISAYIIKKLYIGRSTDEVAL 255
Db 196 AIQSEDMTSFDPKIGLHFGNLFYFLSLSTFLGVGIGLLCAYIIKKLYIGRSTDEVAL 255
QY 256 MMLMAYLSYMLAEELDLGSLITVFFCGIVMSHYTHWNTTESSRVTTKHAFATLSFAETFF 315
Db 256 MMLMSYLSYMAELFYLSGILTVFFCGIVMSHYTHWNTTESSRVTTRHSFATLSFAETFF 315
QY 316 FLVYVGMADLDIEKWEFASDRPKSIGISILLGLVLIGRAAFVPLSLSLNLTKKAPNE 375
Db 316 FLVYVGMADLDIEKWKFKVNSQGLSVAVSSILVGLILVGRAAFVPLSLSLNLTAKNSD 375
QY 376 KITRQOVVIMWAGLMRGAVSIATLAYNKFTSRGHTQLHGNAMITSTITVVLFTSMVFGM 435
Db 376 KISFRQIIIMWAGLMRGAVSIATLAYNKFTSTGHTSLHENAIMITSTVTVVLFTSVVFG 435
QY 436 MTKPLIRILLP-----ASGHP--VTSEPPSKSLHSPLLTSMQGSDELEST--NIVRPSS 486
Db 436 MTKPLINILLPPHKQMPGSHSMITSEPPSKHFTVPLLDNQPDSESDMITGPEVARPTA 495
QY 487 LRMLLTKTPTHTVYVYWRKFDALMRPFGRGVPFPGSPTEQS 531
Db 496 LRMLLTPTHTVYVYWRKFDALMRPFGRGVPFPGSPTEQS 540

RESULT 6
AAY40901
ID AAY40901 standard; Protein: 538 AA.
XX
AC AAY40901;
XX
DT 18-JAN-2000 (first entry)
XX
DE Arabidopsis thaliana Na/H transporter AtNHX1.
XX
KW Sodium; proton; antiport; transporter; salt tolerance; salt management;
KW transgenic plant; survival; soil; farming; accumulation; irrigation;
KW crop.
XX
OS Arabidopsis thaliana.
XX
PN WO9947679-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-CA00219.
XX
PR 18-MAR-1998; 98US-0078474.
PR 15-JAN-1999; 99US-0116111.
XX
PA (BLUM/) BLUMWALD E.
PA (APSE/) APSE M.
PA (SNED/) SNEDDEN W.
PA (AHAR/) AHARON G.
XX
PI Blumwald E, Apse M, Snedden W, Aharon G;
XX
DR WPI: 1999-571840/48.
DR N-PSDB: AAZ22591.
XX
PT Nucleic acid molecules encoding sodium/proton transport polypeptides,
PT useful in genetic engineering salt tolerance in crop plants
XX
PS Claim 36; Fig 1A; 93pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding
CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
CC and capable of increasing salt tolerance in a cell. This sequence
CC corresponds to the AtNHX1 transporter from Arabidopsis thaliana.
CC The Na/H transporter polypeptides provide a means of intracellular
CC salt management, particularly in plants. The sequences are useful for
CC producing transgenic plants that are capable of surviving in soil with
CC high salt levels that would normally inhibit growth of the crop species.

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This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, aridplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.

Sequence 538 AA:

Query Match	74.3%;	Score 2023.5;	DB 20;	Length 538;
Best Local Similarity	73.3%;	Pred. No. 5.6e-199;		
Matches 389;	Conservative	60;	Mismatches 79;	Indels 3;
				Gaps 2;

Qy	3	MEVAAARLGA	LYTTS	DYAS	VSVS	INL	FVALL	CACIV	LGHLEEN	RWN	VNESI	TAL	IGL	CTG	52
Db	2	LDSLVSKP	SL -	STSO	AS	VANL	FEALL	CACIV	LGHLEEN	RWN	MNESI	TAL	IGL	GVG	60
Qy	63	WVILLMTK	GKSS	HLF	VFSE	DP	FIY	LLP	PIIF	NAG	QVKK	KOFF	FRN	FM	122
Db	61	VTILLISK	GSS	HLF	VFSE	DP	FIY	LLP	PIIF	NAG	QVKK	KOFF	FRN	FM	120
Qy	123	SFFTIST	AAIA	IFSR	NIG	TPL	DVGD	FLA	TGA	IFS	ATS	D	S	VCT	182
Db	121	SCTIISL	GV	QFF	K	LDIG	TF	D	GLD	YLA	IGA	IF	AA	F	180
Qy	183	GVYND	ATS	I	V	LEN	AL	Q	N	F	D	L	V	H	242
Db	181	GVYND	ATS	I	V	LEN	AL	Q	N	F	D	L	V	H	240
Qy	243	YIGRHS	T	D	R	E	V	A	L	M	L	M	A	I	302
Db	241	YFGRHS	T	D	R	E	V	A	L	M	L	M	A	I	300
Qy	303	HAFATL	S	F	I	A	E	T	F	L	V	G	M	D	362
Db	301	HTFATL	S	F	I	A	E	T	F	L	V	G	M	D	360
Qy	363	SFLSNL	T	K	A	P	E	K	I	N	F	M	Q	V	422
Db	361	SFLSNL	A	K	K	N	O	S	E	K	I	N	F	M	420
Qy	423	ITVVLF	S	T	M	V	F	G	M	T	K	P	L	I	480
Db	421	ITVCLF	S	T	M	V	F	G	M	T	K	P	L	I	480
Qy	481	IVRESS	R	M	L	T	K	P	H	V	Y	W	R	K	531
Db	481	VPRD	S	R	G	E	L	T	R	V	Y	W	R	O	531

RESULT 7
AAB73254
ID AAB73254 standard; Protein: 555 AA.

AA
AC AAB73254:

DT 14-MAY-2001 (first entry)

DE protein regulating the pH of vacuoles.

vacuole pH regulation: flower colour.

XX
05
Torenia hybrida.

XX PN WO200114560-A1

XX
PD
01-MAR-2001

XX PF 24-AUG-2000: 2000WO-JP05722.

XX
PR 24-AUG-1999: 99JP-0236800.

PA (SUNR) SUNTORY LTD.

Iida S, Tanaka S, Inagaki Y;

DR WPI; 2001-191648/19.

DR N- F3DB, AAF / J700 :
XX

PT morning glory originated gene encoding a protein with an regulatory
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture -

XX
PS
Example 7: Page 57-60: 68pp: Japanese.

The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.

XX	Sequence	555 AA:
SQ		

	Query Match	Score 1966;	DB 22;	Length 555;
Best Local Similarity	71.3%	Pred. No. 4.8e-193;		
Matches 390.	Conservative	55; Mismatches	84;	
		Indels	18;	
				Gaps 5;

Qy	1	MGHE----	VAAARGLALYTTSDYASVVSINL	FVALLCACIVLGHLEENRWNESITALI	56
			: :	: :	
			: :	: :	
Dp	1	MGFEVSIKLAASETDNIW-	SSGSGSVATTFTVLTCTCIVIGHLLPENRWNESITALI	59	

Qy 57 IGLCTGVILLMTKCKSSHLFVSEDIFFIYLLPPIINAGFOVKKKQFFRNFMTITLFG 116
||| |||:: |||| | |||| | |||| | |||| | |||| | |||| | |||| : ||
Dh 60 IGATGVIIILISGKSSHLFVSEDIFFIYALPPPIINAGFOVKKKSFRRNFATIMWFG 119

[illegible]

Qy	177	SLVFGEVVNDATSVLFLNALQNFDLVHIDAAVVKFLCNGFFYLFSLSTGLGVFAGLLSA	2366
		: :	
		:	
Db	179	SLVFGEVVNDATSVVLFNVAQNFDLPHMSTAKAFELVGNFFYLFATSTVLGVTGLLSA	2388

Qy		237 YIHKKLYIGHSTDRVALMMLMAYLSYMLELDDLGLILTVFFCGIVMSHYTHNVNTE	296
		: :	:
Dd		239 YIIKKLYFGHSTDREVAIMTLMAYLSYMAELFDLSGILTVPFCGIVMSHYTHNVNTEN	298

QY 297 SRVTTKHAFTLSFAETFLFYLVGMALDIEKWEFASDRPGKSTIGSSILLGLVLIGRA 356
||||| ||||| :| :||||||| ||| | :| :||||| :|
db 299 SRVTTKHTATLSFAEIFLYLVGMALDIEKWFVSGMNTSAAVSATLLGLVLLSRA 358

QY 357 AFVPLSFSLNLTKKAPNEKITWRQQVVIWAGLMRGVSIALAYNKFTRSHTQLHGNA 416
||||| |||| | ||| : ||||| ||||| : ||| | ||
Db 359 AFVPEPSFSLNIAKKSPIEKISIROOTIIWAGIMRGVSMALAYKOFTRGLTVVERENA 418

Qy 417 IMITSTIVVLFSTWVGMMTKPLIRLLPAS--GHPVTSEPSSPKSLHSPL----- 466

p 419 IETSTTIVFSTWVGIMKPKIINILPSPKINRSVSSEPLTPNSITIPILGESDSV 478

Qy 467 --LTSMQGSDLESTNIVRPSLSRLMLLTKPTHTVHYVYWRKEDDALMRPMFCGRGCVDFSP 524

Dh 470 AEFESTPGOSQCGGPDVAPDSISRLT1TKPTHTVHYVYWRKFDNAEMRPVFGSGRGCVDFVVP 538

07 525 CSDTEOS 531

530 CSDTDC 545
||||:|

RESULT 8
AAY40905
ID AAY40905 standard; Protein; 547 AA.

AA
AC
AAAY40905;

```

XX DT 18-JAN-2000 (first entry)
XX DE Arabidopsis thaliana Na/H transporter.
XX KW Sodium; proton; antiport; transporter; salt tolerance; salt management;
XX KW transgenic plant; survival; soil; farming; accumulation; irrigation;
XX KW crop.
XX OS Arabidopsis thaliana.
XX PN W09947679-A2.
XX PD 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-CA00219.
XX PR 18-MAR-1998; 98US-0078474.
XX PR 15-JAN-1999; 99US-0116111.
XX PA (BLUM/) BLUMWALD E.
XX PA (APSE/) APSE M.
XX PA (SNED/) SNEDDEN W.
XX PA (AHAR/) AHARON G.
XX PI Blumwald E, Apse M, Snedden W, Aharon G;
XX DR WPI; 1999-571840/48.
XX DR N-PSDB; AAZ22595.
XX
XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
XX useful in genetic engineering salt tolerance in crop plants -
XX Claim 50; Fig 5A-B; 93pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding
XX a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
XX and capable of increasing salt tolerance in a cell. This sequence
XX corresponds to a transporter from Arabidopsis thaliana.
XX The Na/H transporter polypeptides provide a means of intracellular
XX salt management, particularly in plants. The sequences are useful for
XX producing transgenic plants that are capable of surviving in soil with
XX high levels that would normally inhibit growth of the crop species.
XX This would be useful in farming land in areas that are generally
XX considered unproductive through salt accumulation and poor irrigation,
XX e.g. in India, Australia, and prairies in USA or Canada. Commercial
XX crops, such as potatoes, tomatoes, brassica, cotton, sunflower,
XX strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
XX atriplex, sorghum, alfalfa, salicornia and others would benefit from
XX increased salt tolerance.
XX
XX Sequence 547 AA;
XX
XX Query Match 68.1%; Score 1852.5; DB 20; Length 547;
XX Best Local Similarity 72.9%; Pred. NO. 2.2e-181;
XX Matches 361; Conservative 55; Mismatches 76; Indels 3; Gaps 2;
XX
XX 3 MEVAAARIGALYTTSDYASVVSINLFAVLLCIVGLHLLLENRWVNESITALLIGLGTG 62
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 2 LDSLVKLPSL-STSDHSSVVALNLFVALLCIVGLHLLLENRWVNESITALLIGLGTG 60
XX
XX 63 VVILMTKGKSHLFFVSEDLFFIYLLPPIIFNAGFQVKKQFFNFMTITLFGAVGTMI 122
XX I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 61 VTILLISKGKSHLFFVSEDLFFIYLLPPIIFNAGFQVKKQFFNFMTITLFGAVGTII 120
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 123 SFFITISAAIAIFRMNIGTLDVGDFAIGAIFGATDSVCTQLVQNDDETPFLYSLVFG 182
XX I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 121 SCTIISLGVTOFFKKLDIGTDLGDYLAIGAIFAATDSVCTQLVQNDDETPFLYSLVFG 180
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 183 GVNNDATSVLNFALQNFDLVHIDAADVLFKLGNFYFLLSSTFLGFAGLLSAYIKKL 242
XX I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 181 GVNNDATSVVFNFAIQSFDLTHLNEAFAHLGNFLYFLLSLTLGGAATGLISAYIKKL 240
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX
XX RESULT 9
XX AAU02882
XX ID AAU02882 standard; Protein; 571 AA.
XX AC AAU02882;
XX DT 12-SEP-2001 (first entry)
XX DE Arabidopsis thaliana AtNHX1 polypeptide.
XX KW AtNHX1; tonoplast pyrophosphatase hydrogen ion translocating pump; AVPI;
XX KW vacuolar pyrophosphatase; salt tolerance; drought tolerance; cation;
XX KW freeze tolerance; 35S promoter; sodium; calcium; manganese; lead;
XX KW saline soil; thale-cress.
XX OS Arabidopsis thaliana.
XX PN W0200133945-AL.
XX PD 17-MAY-2001.
XX PF 10-NOV-2000; 2000WO-US30955.
XX PR 10-NOV-1999; 99US-0164808.
XX PR 18-AUG-2000; 2000US-0226223.
XX PR 22-AUG-2000; 2000US-0644039.
XX PA (UYCO-) UNIV CONNECTICUT.
XX PA (WHED) WHITEHEAD INST.
XX PI Galola RA;
XX WPI; 2001-328862/34.
XX
XX Transgenic plants with salt tolerance, drought and freeze resistance
XX and increased yield and flower size comprise exogenous H+ genes or
XX increased vacuolar pyrophosphatase expression -
XX Example 1; Fig 6; 68pp; English.
XX
XX The sequence represents an Arabidopsis thaliana AtNHX1 polypeptide which
XX is a tonoplast pyrophosphatase hydrogen ion (H+) translocating pump.
XX Transgenic plants can be made by transforming plant cells with exogenous
XX tonoplast pyrophosphatase driven H+ pump genes and an exogenous nucleic
XX acid encoding a protein, such as AVPI, which alters expression of
XX vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant
XX via transformation of the cells to induce upregulation of vacuolar
XX phosphatase expression. Drought and/or freeze tolerance may also be
XX introduced through transformation with DNA encoding a vacuolar H+
XX translocating pump linked to a promoter such as the 35S promoter. These
XX processes are useful for bioremediating soil and removing cations such as
XX sodium, calcium, manganese and lead from soil or water which can

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CC support plant growth. Plants which grow in saline soil can be produced
 CC and yield and flower size of plants can be increased.

XX Sequence 571 AA;

Query Match 66.1%; Score 1799.5; DB 22; Length 571;

Best Local Similarity 68.3%; Pred. No. 6.6e-176; Indels 7; Gaps 4;

Matches 364; Conservative 62; Mismatches 100;

Qy 3 MEVAARLALYTTSDYASVVSINLFCVALLCACIVLGHLLLEENRWVNESITALLIGCTG 62

Db 2 LDSLVSKLPSTLSTDSHASVVALPVALLCACIVLGHLLSSNMWKSITALLIGLCTG 60

Qy 63 VVILMTKSSHLFVSEDEFFIYLLPPIIFNAGFOVKKQFFRNFTITLFCAGVTMI 122

Db 61 VTILLISKSKSHLLFVSEDEFFIYLLPPIIFNAGFOVKKQFFRNFTITLFCAGVTII 120

Qy 123 SFFETISAAIAIFSRMNTIGTLDVDFLAIGAIFATSQVCTQLVNLQDETFFLYSLVFE 182

Db 121 SCTIISLCVTOFPKLDIGTDFLDCYLAICAIFAATSVCTQLVNLQDETFFLYSLVFE 180

Qy 183 GVNWDATSVLNFALQNFDLVHDAAYVVKLFNGFFYLFSSSTFLGVFAGLLSAYIIKKL 242

Db 181 CVVNDATSVVVFNAIQSFDTLHNRHAAFLHLCNLFYLLSTLLGAATCLISAYVIKKL 240

Qy 243 YIGRHSTDRVALMMLMAYLSYMLAELDLSCILTVFCGIVMSHYTHNVTSSRVTK 302

Db 241 YFCHRSTDRVALMMLMAYLSYMLARFLDLSCILTVFCGIVMSHYTHNVTSSRVTK 300

Qy 303 HAFATLSIAETFLFYGMADLDEKWEFASDRPGSIGISILLGLVLGLRAAFVPL 362

Db 301 HTFATLSIAETFLFYGMADLDEKWEFASDRPGSIGISILLGLVLGLRAAFVPL 360

Qy 363 SFLSNLTAKNEKTPWQQVYVWAGLMRGAVSIALAYNFKTRSGHTOLHGNMITS 422

Db 361 SFLSNLAKNOSRKTFNFKVQVYVWAGLMRGAVSIALAYNFKTRSGHTOLHGNMITS 420

Qy 423 ITVLFSTVWFGMTKPLIRLLPASGHPVT--SEPSSPKSLRSPHLLTSMOGSDLEST- 479

Db 421 ITVLFSTVWFGMTKPLIRLLPASGHPVT--SEPSSPKSLRSPHLLTSMOGSDLEST- 478

Qy 480 -NVRPSSRLMLLTKPTHTVHYWRKFDLALMRPMFGGRGVFPSPGSPTEQS 531

Db 479 HNVPRPDSIRGLTRPTVHYWRKFDLALMRPMFGGRGVFPSPGSPTEQS 531

RESULT 10

AAU78424

XX AAU78424 standard; Protein: 556 AA.

XX AAU78424;

XX 18-JUN-2002 (first entry)

XX Physcomitrella patens Na+/H+ antiporter PpNHX1.

XX Plant; Na+/H+ antiporter; PpNHX1; expressed sequence tag; EST;

XX plant protectant; cytosolic; stress tolerance; plant defence activity;

XX canker; gall; tumour; appressorium; pathogenic stress; herbicide;

XX insecticide; acid rain; drought tolerance; plant hormone synthesis;

XX ultraviolet tolerance; flower development; terpene synthesis;

XX plant organoleptic.

XX Physcomitrella patens.

OS W0200216423-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26550.

XX 25-AUG-2000; 2000US-227974P.

XX

PA (BADI) BASF PLANT SCI GMBH.

XX Da Costa Silva EO, Ishitani M;

XX WPI: 2002-292058/33.

XX New Na+/H+ antiporter nucleic acids and proteins, useful e.g. for

XX modulating stress tolerance in plants, or for detecting, preventing,

XX conferring resistance to or treating hyperproliferative diseases, e.g.

XX cankers, galls or tumours

XX Claim 1; Fig 3; 204pp; English.

XX The invention relates to novel isolated Na+/H+ antiporter coding nucleic

XX acid (I) and polypeptides (II). (I) and (II) are useful in modulating the

XX stress tolerance in a plant, preferably modulating a plant's tolerance

XX to limited or inadequate water availability, excess salt or osmotic

XX conditions, excess temperature conditions, excess metal concentration

XX in soil or water, chemical stress and oxidative stress. These may also

XX be used as carbon, nitrogen or carbohydrate source, in modulating plant

XX defence activity, signal transduction, or metabolite transport; or as

XX probes for the identification and isolation of full length cDNAs or

XX genomic DNA. The polynucleotides or polypeptides are further used to

XX detect, prevent, confer resistance to and/or treat hyperproliferative

XX diseases such as cankers, galls, tumours, and appressorium, increase

XX plant defence mechanisms against environmental or pathogenic stresses

XX (e.g. viral, fungal, mycoplasma, bacterial, nematode, herbicidal,

XX insecticidal, acid rain, drought, or chemical), and hormone synthesis.

XX The Na+/H+ antiporter coding nucleic acids can be used in creating

XX transgenic plants with desirable traits, including enhanced plant

XX enhanced flower development and terpene synthesis, in expressing

XX recombinant proteins to raise antibodies against polypeptides, as

XX markers for tissues in which the corresponding protein is expressed, as

XX chromosome markers or tags for chromosome mapping, and for genetic

XX fingerprinting. The polypeptides are useful in the identification,

XX prevention, and/or conferment of resistance to plant diseases,

XX particularly those associated with modulating environmental stress

XX responses, such as drought, freezing and salt tolerance. The polypeptides

XX are further useful in modulating plant yield, development,

XX differentiation, root growth, root morphology, plant colour, plant aroma,

XX plant flavour, palatability of plant tissue, plant organoleptic

XX properties, ability to serve as plant nutraceutical, pharmaceutical or

XX phytochemical, ability to produce nutraceutical, pharmaceuticals or

XX phytochemicals of either endogenous or exogenous origin. Antibodies may

XX be used in diagnostic assays to detect the presence or quantity of the

XX polypeptides, in affinity purification of the polypeptides from

XX recombinant cell culture or natural sources, and for inhibiting allergic

XX reactions in animals. The present sequence represents Physcomitrella

XX patens Na+/H+ antiporter PpNHX1.

XX Sequence 556 AA;

XX Query Match 57.0%; Score 1550.5; DB 23; Length 556;

XX Best Local Similarity 60.9%; Pred. No. 2.6e-150;

XX Matches 316; Conservative 66; Mismatches 116; Indels 21; Gaps 7;

Qy 18 DYASVWSINIFVALLCACIVLGHLLLEENRWVNESITALLIGCTGVILLMTKSSHLF 77

Db 23 DRIDVISICLVFLLCACIVLGHLLLEENRWVNESITALLIGLFTGSIVLLSSKQGSIL 82

Qy 78 VSEDLFFIYLLPPIIFNAGFOVKKQFFRNFTITLFGAVGTMTSFTTISIAAIAFTR 137

Db 83 EFDEELFFIYLLPPIIFNAGFOVKKQFFRNFTITLFGAVGTMTSFTTISIAAIAFTR 142

Qy 138 MNIGTLDVGDFLAIGFATSQVCTQLVNLQDETFFLYSLVFGGVNDATSLVFNAL 197

Db 143 FGLKNLPTRDILAIQVIFATSQVCTQLVNLQDETFFLYSLVFGGVNDATSLVFNAL 202

Qy 198 QNEDLVHIDAADVILKGNFFYLLFSLSTFLGVFAGLLSAYIIKKLYTIGRSTDEVALMM 257

Db 203 QTYNPDNFTSLGIGGFLYLLFSSCILGASGLISAYIIKTYFGRSTDEIRAINT 262

QY 258 LMAYLSYMLAELLDLSGLTVFFCGIVMSHYTHWNTSSRVTTKHAFATLSFAETFLF 317
 Db 263 LMAYLSYFAELFYLGLSLVFFCGIVMSHYTHWNTSSRVTTKHAFATLSFAETFLF 322
 QY 318 LYVGMDALDIEKWEFASDRPKSIGISSILGLVLIGRAAFVPLSLNLTKKAPNEKI 377
 Db 323 LYVGMDALDIEKWEFASDRPKSIGISSILGLVLIGRAAFVPLSLNLTKKAPNEKI 381
 QY 378 TWROQVVIWAGLMRGAVSIALAYNKKFTSRGHTQLHGNAMITSTITVVLSTWVFGHMT 437
 Db 382 NLRQVVIWAGLMRGAVSIALAFN--QGDAKDSNQATLMVITIIIVLESTVFGTAT 438
 QY 438 KPLRLLLPASGHVPTSPS--SPKS-----LHSPLLTSMQGSLE----STTNIVR--- 483
 Db 439 KPLSLWLLPFRFNSYSDASLSPKASLDADFHIPLMLDTEREELEANDRSTINQILNGL 498
 QY 484 --PSSRLMLTKPHTVHYWYKFDALRPMFGGRGV 520
 Db 499 PCPOSIGMLLTAPRSTIHWV-KFDDSYMRPTFGRGYV 536

RESULT 11
 ID AAY40902 standard; Protein: 529 AA.
 XX AC AAY40902;
 XX 18-JAN-2000 (first entry)
 DE Arabidopsis thaliana Na/H transporter AtNHX2.
 KW Sodium; proton; antiport; transporter; salt tolerance; salt management;
 KW transgenic plant; survival; soil; farming; accumulation; irrigation;
 KW crop.
 XX Arabidopsis thaliana.
 XX WO9947679-A2.
 XX 23-SEP-1999.
 XX 18-MAR-1999; 99WO-CA00219.
 XX 18-MAR-1998; 98US-0078474.
 PR 15-JAN-1999; 99US-0116111.
 XX (BLUM/) BLUMWALD E.
 PA (APSE/) APSE M.
 PA (SNED/) SNEDDEN W.
 PA (AHAR/) AHARON G.
 XX Blumwald E, Apse M, Snedden W, Aharon G;
 WPI; 1999-571840/48.
 DR N-PSDB; AA622592.
 XX Nucleic acid molecules encoding sodium/proton transport polypeptides,
 PT useful in genetic engineering salt tolerance in crop plants -
 PS Claim 36; Fig 1B; 93pp; English.
 XX The invention relates to an isolated nucleic acid molecule encoding
 CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment
 CC and capable of increasing salt tolerance in a cell. This sequence
 CC corresponds to the AtNHX2 transporter from Arabidopsis thaliana.
 CC The Na/H transporter polypeptides provide a means of intracellular
 CC salt management, particularly in plants. The sequences are useful for
 CC producing transgenic plants that are capable of surviving in soil with
 CC high salt levels that would normally inhibit growth of the crop species.
 CC This would be useful in farming land in areas that are generally
 CC considered unproductive through salt accumulation and poor irrigation,
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,

CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from
 CC increased salt tolerance.
 XX Sequence 529 AA;
 SQ Query Match 56.2%; Score 1529; DB 20; Length 529;
 Best Local Similarity 58.2%; Pred. No. 3.9e-148;
 Matches 297; Conservative 83; Mismatches 116; Indels 14; Gaps 5;
 QY 17 SDYASVSNIFVALLCACIVLGHLEENRWVNESITALIIGLCGTGVVILLMTKGSKSHL 76
 Db 15 AEHPQVIPSIFVIALCLCLVGHLEENRWVNESITALIIGLCGTGVVILLMTKGSKSHI 74
 QY 77 FVSEDLFFIYLLPIIFNAGFQVKKKOFFRNFMTITILFAGVGTMISFTTISIAAIAPS 136
 Db 75 LVFDEELFFIYLLPIIFNAGFQVKKKFFHNFILTMSFGVIGVFISFGTWLFFP 134
 QY 137 RMNICTLDVGDFLATGALFSATDSVCTLQVLNQDETPELSLVFGGVVNDATSIVLFA 196
 Db 135 KLGFKGLSARDYLAIGTIFSDTIVCTLIQLRQDETPLYLSLVFGGVVNDATSVVLFA 194
 QY 197 LONFDLVHIDAANVLKFLGNFFYFLSFTFLGVFAGLLSAYIIKKLYTGRHSTDEVALM 256
 Db 195 VQKIQFESLTGWTALQVFNFLYLFSTSTLLGIGVGLITSEVLKTLFGRHSTRELAIM 254
 QY 257 MLMAYLSYMLAELLDLSGLTVFFCGIVMSHYTHWNTSSRVTTKHAFATLSFAETFL 316
 Db 255 VLMAYLSYMLAELFSLGILTVFFCGVLMVSHYASVNTSSRITSRHHVAFMLSFATETFI 314
 QY 317 FLYVGMALDIEKWEFASDRPKSIGISSILGLVLIGRAAFVPLSLNLTKK--APN 374
 Db 315 FLYVGTALDFTKWTSSLSFGGTLGVSGVITALLVLLGAAAFVPLSLVLTNFMNRHTERN 374
 QY 375 EKITRQOVVIWAGLMRGAVSIALAYNKKFTSRGHTQLHGNAMITSTITVVLSTWVFG 434
 Db 375 ESITFKHQVVIWAGLMRGAVSIALAFKQFTYSGVTGLDVPVNAAMVTNTIVLFTTIVFG 434
 QY 435 MMTKPLIRLLPASGHPVT-----SEPSPK-SLHSPLLTSMQGSLESTTNIVRP-SS 486
 Db 435 FLTKPLVNYLLPQDASHNTGNRGKTEBFGSPKEDATLPLLS----FDESASTNENRADS 490
 QY 487 LRMLLTPTHTVHYWYKFDALRPMFGG 516
 Db 491 ISLLMEQPVYTIHRYWRKFDFTYMRPIFG 520

RESULT 12
 ID ABG61535 standard; Protein: 671 AA.
 XX AC ABG61535;
 XX 27-AUG-2002 (first entry)
 DE Human transporter and ion channel, TRICH5, Incyte ID 7476938CD1.
 XX Human; transporter and ion channel; TRICH; transport disorder;
 KW neurological disorder; muscle disorder; immunological disorder; cancer;
 KW scleroderma; systemic lupus erythematosus; allergy; leukaemia;
 KW cell proliferative disorder; cervical cancer; breast cancer;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW myotonic dystrophy; catatonina; endocrine disorder; diabetes;
 KW Grave's disease; gastrointestinal disorder; Crohn's disease;
 KW renal disorder; Good pasture's syndrome; viral infection; cirrhosis;
 KW bacterial infection; fungal infection; parasitic infection;
 KW protozoal infection; helminthic infection; cardiovascular disorder;
 KW atherosclerosis; hepatic disease.
 XX Homo sapiens.
 OS WO200204541-A2.
 XX

23-MAY-2002.
25-OCT-2001; 2001WO-US46055.
27-OCT-2000; 2000US-243989P.
03-NOV-2000; 2000US-245904P.
09-NOV-2000; 2000US-247673P.
17-NOV-2000; 2000US-249661P.
20-NOV-2000; 2000US-252232P.
01-DEC-2000; 2000US-250790P.
(INCY-) INCYTE GENOMICS INC.
Tang YT, Yue H, Nguyen DB, Hafalia AJA, Elliott VS, Lu Y;
Walia NK, Yao MG, Baughn MR, Gandhi AR, Ding L, Sanjanwala M;
Ramkumar J, Arvizu C, Gietzen KJ, Lal PG, Azimzai Y, Khan FA;
Thangavelu K, Thornton M, Lu DAM, Tribouley CM, Warren BA;
Ison CH, Das D, Raumann BE, Policky JL, Kearney L;
WPI; 2002-463570/49.
N-PSDB; ABK83214.
New transporters and ion channels (TRICH) polypeptides, useful for
diagnosing, preventing, and treating disorders associated with an
abnormal expression or activity of TRICH, e.g. immunological, muscular
or renal disorders -
Claim 1; Page 138-140; 178pp; English.
The invention relates to human transporters and ion channels (TRICH)
polypeptides, a naturally occurring amino acid sequence 90 % identical to
TRICH, a biologically active fragment of TRICH or an immunogenic fragment
of TRICH. Also included are an isolated polynucleotide encoding TRICH,
a recombinant polynucleotide comprising a promoter sequence operably
linked to the TRICH polynucleotide, a cell transformed with the
recombinant polynucleotide, a transgenic organism comprising the
recombinant polynucleotide, an isolated antibody that binds specifically
to TRICH, and screening for compounds which bind to TRICH, modulate
TRICH, modulate TRICH expression or are ant/agonists of TRICH.
The polypeptides are useful for diagnosing, treating, and
preventing transport, neurological, muscle, immunological disorders
(e.g. scleroderma, systemic lupus erythematosus, allergies), cell
proliferative disorders such as cancers (e.g. leukaemia, cervical or
breast cancers), neurodegenerative disorders (e.g. Parkinson's disease,
Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
catatonias), endocrine disorders (e.g. diabetes, Grave's disease),
gastrointestinal disorders (e.g. Crohn's disease), renal disorders,
(e.g. Good pasture's syndrome), viral, bacterial, fungal, parasitic,
protozoal and helminthic infections, cardiovascular disorders (e.g.
atherosclerosis), or hepatic diseases (e.g. cirrhosis) and many
other diseases and disorders detailed in the specification. They can also
be used in assessing the effects of exogenous compounds on the
expression of nucleic acid and amino acid sequences of transporters and
ion channels. TRICH or its fragments may also be used in screening for
compounds that specifically bind to and modulate the activity of TRICH.
The polynucleotides can be used to create knock-in humanised animals or
transgenic animals to model human disease. The present sequence
represents a TRICH protein.
Sequence 671 AA;
Query Match 22.7%; Score 618; DB 23; Length 671;
Best Local Similarity 31.2%; Pred. No. 2.6e-54;
Matches 174; Conservative 95; Mismatches 22; Indels 56; Gaps 16;
QY 2 GMEVAARALGALYTTSDYASVWSINLFVALLCACIVLGHLLLENR--WYNESITALIIGL 59
DB 129 GKPLVPQTEQQAQEQSSGWTFFSLVLAICILVHLLIRYRLHFLPESVAVVSLG1 188
QY 60 CTGWILLMTKGKSHL----FVSEDLFTIYLLPPIIFNAGFQVKKQKFFRPMITLFG 116
DB 189 LMGAVIKITFEKLANWKEEMPRPNMFFLLLPPIIFESGYSLSHGKNGFNQIGSITLFA 248

QY 117 AVCTMISFETISIAAIAIFSRMNIQGLDVGDLAIGAIFSATDSVCTLOVLNQ--DETPEL 175
DB 249 VFGTAISAFVGGGIYFQGAQVISKLNMTDSFAFGSLISAVDPVATIAIFNALHVDVPL 308
QY 176 YSLVFGGEGVNDATSVLFNALQNFDLVHIDAA-----VVLKFLGNFFYFLSSTFGVFA 231
DB 309 NMLVFGESILNDASVILVNTAEGLTRKNMSDVSGWOTFLQALDYFLKMFSGSAALGTLT 368
QY 232 GLISAVIIKKLYIGRHSIDREVALMMLMAYLSYMLAELLDLSGILTVFFCGIVMSHTWH 291
DB 369 GLISALVYLKHIDL-RKTPSLEFGMMITIFAYLPYGLAEGISLSGIMAILFSGIVMSHYTHH 427
QY 292 NVTESSRVTTKHAFAATLSFIATFELFLYVGMALDI-EKWEFASDRPGKSIGISSIL--L 348
DB 428 NLSFVQILMQOQLRVVAFCECTCVAFGLSLIFSPPHKE-----ISFVIWCI 476
QY 349 GLVLIGRAAEVFLSFLSNLTAKPNEKITWROOVVWAGLMRGAVSALAYNKKTRSG 408
DB 477 VLVLEGRAVNIFFLSYLLNFR---DHKITPKMFMFMFSGSL-RGAIPYAL-----SL 525
QY 409 HTQL---HGNAIMTSTITVVLFTSVVFGMMTKPLIRLLPASGHPVTSEPPSKSLHSP 465
DB 526 HLLEPEMEKROLIGTTTIVIVLFTLILLLGGSTMPILKLM-----DIEDAKAHR 574
QY 466 LLTSMQGSLESTTNIVRPSLSRLMLLTKPHTVHYIYWRK-----FDDALMRPMFEGRG 518
DB 575 NKDVLNLSKTEKMGNTVESEHLSL-LTEEEYEAHYIRRODLKGFVWLDAKYLNPFTRR- 632
QY 519 FVPFSPGSPTEQSHGGR 535
DB 633 -----LTOEDLHHGR 642
RESULT 13
AAB29621
ID AAB29621 standard; Protein; 608 AA.
XX AAB29621;
XX 19-FEB-2001 (first entry)
XX Cat flea HMT Na/H transporter, SEQ ID NO:1868.
XX Cat flea; hindgut and Malpighian tubule protein; HMT;
XX flea infestation; vaccine; antiparasitic; therapeutic target;
XX diagnosis; detection.
XX Ctenocephalides felis.
XX WO2000061621-A2.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-US09437.
XX 09-APR-1999; 99US-0128704.
XX (HESK-) HESKA CORP.
XX Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX WPI; 2000-656323/63.
XX N-PSDB; AAC95370, AAC95371, AAC95372, AAC95373.
XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic
XX acids useful for the prevention, diagnosis and treatment of flea
XX infestations -
XX Claim 10; Page 891-893; 964pp; English.
XX The invention relates to novel cat flea (Ctenocephalides felis) nucleic
XX acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
XX or head and nerve cord (HNC) tissue. The invention also relates to the

CC encoded proteins. The invention additionally encompasses expression
 CC constructs, recombinant viruses and recombinant cells comprising the
 CC nucleic acids of the invention, recombinant production of the proteins,
 CC antibodies against the proteins, a method of identifying inhibitors of
 CC the proteins, and compositions comprising the inhibitors for
 CC administration to an animal. The nucleic acids, and the proteins they
 CC encode may be used in the prevention, treatment and diagnosis of diseases
 CC associated with flea infestations. For example, the nucleic acids may be
 CC used to produce an HMT or HNC protein according to standard recombinant
 CC DNA methodology by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
 CC and quantitate the presence of cat flea or other homologous nucleic acid
 CC sequences in samples. They may also be used to study the expression and
 CC function of the proteins and their role in metabolism. The HMT and HNC
 CC proteins may be used as antigens in the production of specific
 CC antibodies, and in assays to identify modulators (agonists and
 CC antagonists) of HMT and/or HNC protein expression and activity. The
 CC anti-HMT/HNC protein antibodies and antagonists may also be used to
 CC downregulate protein expression and activity. The antibodies may also be
 CC used as diagnostic agents for detecting the presence of flea polypeptides
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
 CC present sequence represents a cat flea HMT protein of the invention.

XX Sequence 608 AA;

Query Match 22.1%; Score 600.5; DB 21; Length 608;
 Best Local Similarity 35.1%; Pred. No. 1.4e-52;
 Matches 153; Conservative 95; Mismatches 153; Indels 35; Gaps 13;

QY 21 SWVSNLFAVALLACIVLGHLEEN--RWVNESITALLIGLCTGVILLMTKGKSSH-- 76
 Db 81 SSMISFFVLCVALLGILLIHFMLOTGFOYLPESIVVFLGALIGLIINLMSSKNIANKN 140
 QY 77 -FVFSDELFFIYLLPPIIFNAGFOVKKQFFRNFTITLFGAVGTMISFFTTISAAIAIF 135
 Db 141 EEAFTPAFFLVLLPPIIFESGYNLHKGNTFONIGSILVFAIFGTAFSAFVVG-AGVILL 199
 QY 136 SRMIG-TLDVGDFLATGAIFSDTSVCTLOVLNO--DETPELYSLVFGGVNDATSVL 193
 Db 200 GMADVAVNLSVESFAGFGLSLISAVDPVATVAIFHALDVPVNLMLVFGESITLDAISIVL 259
 QY 194 FNA-LQNFDLVHDAVAVLKLFGNFFFLSSTFLGVFAGLLSAVIKKLYIGRHSTDR 252
 Db 260 TTALESNNPLMTTAAVSVGLNFCFLMFFASAGVGVFALISALLKHLVDLRKPS-LE 318
 QY 253 VALMMLMAYLSYMLAELDLGILTVFPCGIVMSHYTHWNVTSSRVTTKHAFATLSF 312
 Db 319 LGMMLVFTYAPYVLAEGIHLSGIMAILFCGIVMSHYTHFNLSTVTQITMQOTMRTLAF 378
 QY 313 ETEFLYVGMDDALDIEKWEFASDRPKSGISGILLGLVILGRAAFVPLSFLNLTKA 372
 Db 379 ETCVFAILGMAIFSR-----HRVEPALVTSIV--LCILGRAANIPPLSMLVNFRE- 429
 QY 373 PNEKITRQOVVIMWAGLMRGAVSIALA----YKNKFRSGHTQLHGNAIMTTSTITVLF 428
 Db 430 --HKITKMAIFMWSGL-RGALSIALSLHLEFSDTERH-----VIITTLIIVLC 477
 QY 429 STWVFGMTKPLRL 444
 Db 478 TTLIFGATMPLKFL 493

RESULT 14

ABBS9364

XX ID ABBS9364 standard; Protein: 649 AA.

AC AC ABBS9364;

XX XX

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 4884.

DE

XX

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL03467.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 4884; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBS72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 649 AA;

Query Match 21.9%; Score 595.5; DB 22; Length 649;
 Best Local Similarity 35.1%; Pred. No. 5.1e-52;
 Matches 155; Conservative 88; Mismatches 155; Indels 43; Gaps 15;

QY 24 SINLFVALLACIVLGHLEEN-----RWVNESITALLIGLCTGVILLMT--KGKSSH 75
 Db 101 SLSLFF-VICV-IMGILLIHSMLOTGFOYLPESIVVFLGAFGLSUNVMSGQSGSKR 158
 QY 76 LFVFSDELFFIYLLPPIIFNAGFOVKKQFFRNFTITLFGAVGTMISFFTTISAAIAIF 135
 Db 159 EEVFSPMGFFLVLLPPIIFESGYNLHKGNTFONIGSILVFAIFGTITISALVIG-AGIYLL 217
 QY 136 SRMIG-TLDVGDFLATGAIFSDTSVCTLOVLNO--DETPELYSLVFGGVNDATSVL 193
 Db 218 GLGEVAFRLSFSFAGFGLSLISAVDPVATVAIFHALDVPVNLMLVFGESITLDAISIVL 277
 QY 194 FNALQNFDLVHDAVAVLKLFGNFFFLSSTFLGVFAGLLSAVIKKLYIGRHSTDR 250
 Db 278 TASITQSANVNAEASTGEAMPSALKTCAMFFASAGVGVFALISALLKHLVDLRKPS- 336
 QY 251 REVALMMLMAYLSYMLAELDLGILTVFPCGIVMSHYTHWNVTSSRVTTKHAFATLSF 310
 Db 337 LEFAMLMFTYAPYVLAEGIHLSGIMAILFCGIVMSHYTHFNLSTVTQITMQOTMRTLAF 396
 QY 311 IAEITFLYVGMDDALDIEKWEFASDRPKSGISGILLGLV--LIGRAAFVPLSFLNLT 368
 Db 397 IAEITCVFAILGMAIFSR-----HQVELSFVIAIVLCILGRACNIFPLAFVFN- 445
 QY 369 TKKAPNEKITRQOVVIMWAGLMRGAVSIALAYNKNKFRSGHTQLHGNA---IMTSTTIV 425
 Db 446 --KFRHKINNMKQFIMWFSGL-RGALSIAL-----SLHNLDSQEKRIIVITTLII 495

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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:51:14 ; Search time 28 Seconds
(without alignments)
562.188 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAARLALGALYTTSDYA.....GRGFVPSGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	491	18.0	832	2	US-08-677-734A-12	Sequence 12, Appl
2	491	18.0	832	4	US-09-097-053-12	Sequence 12, Appl
3	482.5	17.7	834	2	US-08-677-734A-9	Sequence 9, Appl
4	482.5	17.7	834	2	US-08-677-734A-10	Sequence 10, Appl
5	482.5	17.7	834	4	US-09-097-053-9	Sequence 9, Appl
6	482.5	17.7	834	4	US-09-097-053-10	Sequence 10, Appl
7	480.5	17.7	831	2	US-08-677-734A-11	Sequence 11, Appl
8	480.5	17.7	831	4	US-09-097-053-11	Sequence 11, Appl
9	200.5	7.4	683	4	US-09-134-001C-5576	Sequence 5576, Ap
10	130.5	4.8	635	2	US-09-014-969-11	Sequence 11, Appl
11	124.5	4.6	605	4	US-09-134-001C-4425	Sequence 4425, Ap
12	118.5	4.4	800	4	US-09-134-001C-5655	Sequence 5655, Ap
13	114	4.2	477	4	US-09-134-001C-3487	Sequence 3487, Ap
14	113	4.2	1394	4	US-09-213-053-2	Sequence 2, Appl
15	111	4.1	650	4	US-08-800-291B-4	Sequence 4, Appl
16	110	4.0	400	4	US-09-134-001C-2912	Sequence 2912, Ap
17	109.5	4.0	617	4	US-09-134-001C-4012	Sequence 4012, Ap
18	109	4.0	222	4	US-09-134-001C-4748	Sequence 4748, Ap
19	109	4.0	649	4	US-08-800-291B-5	Sequence 5, Appl
20	108	4.0	649	4	US-08-800-291B-6	Sequence 6, Appl
21	107.5	3.9	492	4	US-09-134-001C-4847	Sequence 4847, Ap
22	107	3.9	776	4	US-09-165-396-3	Sequence 3, Appl
23	104.5	3.8	518	4	US-09-134-001C-4744	Sequence 4744, Ap
24	103.5	3.8	450	4	US-09-134-001C-4858	Sequence 4858, Ap
25	103	3.8	324	4	US-09-134-001C-5525	Sequence 5525, Ap
26	103	3.8	373	4	US-09-134-001C-4029	Sequence 4029, Ap
27	103	3.8	405	4	US-09-134-001C-4999	Sequence 4999, Ap

28	101.5	3.7	434	2	US-08-529-600D-2	Sequence 2, Appl
29	101.5	3.7	434	2	US-08-973-275-4	Sequence 4, Appl
30	101.5	3.7	434	3	US-09-122-632-2	Sequence 2, Appl
31	99.5	3.7	717	4	US-08-924-629C-5	Sequence 5, Appl
32	99	3.6	525	4	US-09-351-224E-8	Sequence 8, Appl
33	97.5	3.6	530	4	US-09-134-001C-4510	Sequence 4510, Ap
34	97	3.6	2496	4	US-09-125-028-2	Sequence 2, Appl
35	96.5	3.5	299	2	US-09-097-759-3	Sequence 3, Appl
36	96.5	3.5	306	2	US-09-097-759-2	Sequence 2, Appl
37	96.5	3.5	462	2	US-08-898-976-2	Sequence 2, Appl
38	96.5	3.5	462	2	US-08-898-976-4	Sequence 4, Appl
39	96	3.5	506	4	US-09-066-047-7	Sequence 7, Appl
40	96	3.5	2958	4	US-08-894-344C-2	Sequence 2, Appl
41	95.5	3.5	438	2	US-08-677-049-9	Sequence 9, Appl
42	95.5	3.5	504	4	US-09-134-001C-5530	Sequence 5530, Ap
43	95.5	3.5	766	4	US-09-134-001C-3689	Sequence 3689, Ap
44	94	3.5	266	2	US-08-225-480-7	Sequence 7, Appl
45	94	3.5	266	2	US-09-097-759-4	Sequence 4, Appl

ALIGNMENTS

1

RESULT 1

US-08-677-734A-12

; Sequence 12, Application US/08677734A

; Patent No. 5871919

; GENERAL INFORMATION:

; APPLICANT: Brant, Steven R.

; APPLICANT: Yun, Chris C.H.

; APPLICANT: Donowitz, Mark

; APPLICANT: Tse, Chung-Ming

; TITLE OF INVENTION: Cloning, Tissue Distribution, and

; TITLE OF INVENTION: Functional Analysis Of The Human Na⁺/B⁺ Exchanger Isoform,

; TITLE OF INVENTION: NHE3.

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/677,734A

; FILING DATE: 10-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B.

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0043-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 832 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-677-734A-12

Query Match 18.0%; Score 491; DB 2; Length 832;

Best Local Similarity 31.7%; Pred No. 5,4e-39;

Matches 145; Conservative 88; Mismatches 172; Indels 52; Gaps 18;

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QY 25 INLFVALLCACIVLGHLLLE-NRWVNESITALLIGLCTGVWILLMTKGKSSHL--VFVSE 81
Db 57 IALWLVASIAKIVFHLSHKVTSPVPSALLIVGLVGLGIVL-----AADHIASFTLTP 111
QY 82 DLFYIYLLPPIIFNAGFOVKKKOFFNEMTITLFGAVGTMISFTTISIAAIAIFSRMNI 141
Db 112 TVFFFYLLPPIVDAGYFMPNRLFFSNLGSILLIYAVVGTWNAATTGLSLYGVFLSGIMG 171
QY 142 TLDVG--DELAICAFSATSCTLOVLAQ-DETPFLYSLVFGGVVNDATSIIVFNALQ 198
Db 172 ELKIGLDELFLGSLIAADVPVAVLAVFEVHVNEVLFITVFGESLNDVAVTVLYNVFQ 231
QY 199 NFDLVHIDAAV--VLKFLGNFEYFLSSTFLG-VFAGLLSAYIIKKLYIGHRSTDEVA 254
Db 232 SFTVLGGDKVTGDCVKGVISFFVSLGTLGVGVFAFLS--LVTR--FTKHVRVIEPG 287
QY 255 LMLMAYLSYMLAEILLDLGILTVFCGIVMSHYTHWNTVTSRVTTKHAFATLSFIAT 314
Db 288 FVFIISYLSYLTSEMLSSILAITFCGICCOKYKANISEQSATTVRYTMKMLASGAET 347
QY 315 FLFLYVGMDALD--TEKWEFASDRPKSGTIGSILLGLVIGRAAFVFLPSLSNLTCKA 372
Db 348 IIFMFLGISAVDPLIWTWNTAFVR-----LTLFVSVFRATGVVLQTLNLRMYV 398
QY 373 PNEKITWROQVVIWAGLMRGAVSIALAYNKFTRSHTQLHGNAI----MITSTIVTVLF 428
Db 399 QLELI---DQVVMSSYGLL-RGAVAFALV-----ALLDGNKYKKNLFTVSTIIVVF 445

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RESULT 2

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US-09-097-053-12
; Sequence 12, Application US/09097053
; Patent No. 6392025
; GENERAL INFORMATION:
; APPLICANT: Brant, Steven R.
; APPLICANT: Yun, Chris C.H.
; APPLICANT: Donowitz, Mark
; APPLICANT: Tse, Chung-Ming
; TITLE OF INVENTION: Cloning, Tissue Distribution, and
; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097.053
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/677,734
; FILING DATE: 10-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0043-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400

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; INFORMATION FOR SEQ ID NO: 12:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-097-053-12

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Query Match

18.0%; Score 491; DB 4; Length 832;

Best Local Similarity 31.7%; Pred. No. 5.4e-39;

Matches 145; Conservative 88; Mismatches 172; Indels 52; Gaps 18;

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QY 25 INLFVALLCACIVLGHLLLE-NRWVNESITALLIGLCTGVWILLMTKGKSSHL--VFVSE 81
Db 57 IALWLVASIAKIVFHLSHKVTSPVPSALLIVGLVGLGIVL-----AADHIASFTLTP 111
QY 82 DLFYIYLLPPIIFNAGFOVKKKOFFNEMTITLFGAVGTMISFTTISIAAIAIFSRMNI 141
Db 112 TVFFFYLLPPIVDAGYFMPNRLFFSNLGSILLIYAVVGTWNAATTGLSLYGVFLSGIMG 171
QY 142 TLDVG--DELAICAFSATSCTLOVLAQ-DETPFLYSLVFGGVVNDATSIIVFNALQ 198
Db 172 ELKIGLDELFLGSLIAADVPVAVLAVFEVHVNEVLFITVFGESLNDVAVTVLYNVFQ 231
QY 199 NFDLVHIDAAV--VLKFLGNFEYFLSSTFLG-VFAGLLSAYIIKKLYIGHRSTDEVA 254
Db 232 SFTVLGGDKVTGDCVKGVISFFVSLGTLGVGVFAFLS--LVTR--FTKHVRVIEPG 287
QY 255 LMLMAYLSYMLAEILLDLGILTVFCGIVMSHYTHWNTVTSRVTTKHAFATLSFIAT 314
Db 288 FVFIISYLSYLTSEMLSSILAITFCGICCOKYKANISEQSATTVRYTMKMLASGAET 347
QY 315 FLFLYVGMDALD--TEKWEFASDRPKSGTIGSILLGLVIGRAAFVFLPSLSNLTCKA 372
Db 348 IIFMFLGISAVDPLIWTWNTAFVR-----LTLFVSVFRATGVVLQTLNLRMYV 398
QY 373 PNEKITWROQVVIWAGLMRGAVSIALAYNKFTRSHTQLHGNAI----MITSTIVTVLF 428
Db 399 QLELI---DQVVMSSYGLL-RGAVAFALV-----ALLDGNKYKKNLFTVSTIIVVF 445
QY 429 STMVF-GMKTPLIR-LLLPASGHPVTSEPPSPKSLH 463
Db 446 FTVIFOGTLTKPLVQMLVKRSEH---REPKNLEKLH 479

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RESULT 3

US-08-677-734A-9

; Sequence 9, Application US/08677734A

; Patent No. 5871919

; GENERAL INFORMATION:

; APPLICANT: Brant, Steven R.

; APPLICANT: Yun, Chris C.H.

; APPLICANT: Donowitz, Mark

; APPLICANT: Tse, Chung-Ming

; TITLE OF INVENTION: Cloning, Tissue Distribution, and

; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677,734A
 FILING DATE: 10-JUL-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fordis, Jean B.
 REGISTRATION NUMBER: 32,984
 REFERENCE/DOCKET NUMBER: 05387,0043-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-677-734A-9

Query Match 17.7%; Score 482.5; DB 2; Length 834;
 Best Local Similarity 31.4%; Pred. No. 3.6e-38;
 Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;

QY 48 VNESITALIIGCTGVVILLMTKGSNHL--FVSEDLFFIYLLPPIIFNAGFQVKKQF 105
 DB 82 VPESALLIVLGLVGGIV----WAADHIASTLTPTVFFVYLLPIVLDAGYFMPNRLF 136
 QY 106 FRNFWTITLFGAVGTMISFFTTISIAAIAIFSRMNIPTDVG--DFAIGAIFSATDSVCT 163
 DB 137 FGNLGTILLYAVGVTVNNAATGSLYGVFLSGLMGDLQIGLLDFLLFGLSMAAIVDPVAV 196
 QY 164 LOVLNQ--DETPLYSLVFGGVNDATSIPLFNALQNFDLV---HIDAIVLKLFGNFFY 219
 DB 197 LAVFEVHVNEVLFIIVFGESLNDATVVLVNFVSFVALGDNVTGVCVKGISVDFV 256
 QY 220 LFLSSTFLG--VFAGLLSAYIIKKLYIGRSTDRVALMMLMAYLSYLAELLDLSGLTV 278
 DB 257 VSLGGLTVGVVFAFLLS--LVTR--FTKHVRIIEPGFVFIISYLSYLSLSEMLSLAILAI 312
 QY 279 FFCGIVMSHYTHWNTSESSRVTTKHAFAFATLSFIAETFLFYVGMMDALDIEKWEFASDRPG 338
 DB 313 TFCGICCCQYKVNISEQSAITVRYTMKMLASSAETIIFMFLGISAVNPFITW----- 366
 QY 339 KSIGISSILLGLVLIG--RAAFVFPFLSFLSNLTKKAPNEKITWROOVVIMWAGLMRGAVS 396
 DB 367 ---NTAFVLLTVFISYRAIGVLOTWLLNRYRMVQLEPI---DOVVLSTYGGGL-RGAVA 419
 QY 397 IALAYNKFTSRGHTOLHGNAI---MITSTIVVLFSTWVF--GMMTKPLIR--LLLPASGH 450
 DB 420 FALV-----VLLDGKVKKEKMLFVSTTIIVVFTVIFQGLTIKPLVQWLKVRSEH 470
 QY 451 PVTSEPPSPKSLH 463
 DB 471 ---REPRNLNEKLH 480

RESULT 4
 US-08-677-734A-10
 Sequence 10, Application US/08677734A
 Patent No. 5871919

GENERAL INFORMATION:
 APPLICANT: Brant, Steven R.
 APPLICANT: Yun, Chris C.H.
 APPLICANT: Donowitz, Mark
 APPLICANT: Tse, Chung-Ming
 TITLE OF INVENTION: Cloning, Tissue Distribution, and
 Functional Analysis Of The Human Nat/H+ Exchanger Isoform,
 NHE3.
 TITLE OF INVENTION: NHE3.
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/677,734A
 FILING DATE: 10-JUL-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fordis, Jean B.
 REGISTRATION NUMBER: 32,984
 REFERENCE/DOCKET NUMBER: 05387,0043-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-677-734A-10

Query Match 17.7%; Score 482.5; DB 2; Length 834;
 Best Local Similarity 31.4%; Pred. No. 3.6e-38;
 Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;

QY 48 VNESITALIIGCTGVVILLMTKGSNHL--FVSEDLFFIYLLPPIIFNAGFQVKKQF 105
 DB 82 VPESALLIVLGLVGGIV----WAADHIASTLTPTVFFVYLLPIVLDAGYFMPNRLF 136
 QY 106 FRNFWTITLFGAVGTMISFFTTISIAAIAIFSRMNIPTDVG--DFAIGAIFSATDSVCT 163
 DB 137 FGNLGTILLYAVGVTVNNAATGSLYGVFLSGLMGDLQIGLLDFLLFGLSMAAIVDPVAV 196
 QY 164 LOVLNQ--DETPLYSLVFGGVNDATSIPLFNALQNFDLV---HIDAIVLKLFGNFFY 219
 DB 197 LAVFEVHVNEVLFIIVFGESLNDATVVLVNFVSFVALGDNVTGVCVKGISVDFV 256
 QY 220 LFLSSTFLG--VFAGLLSAYIIKKLYIGRSTDRVALMMLMAYLSYLAELLDLSGLTV 278
 DB 257 VSLGGLTVGVVFAFLLS--LVTR--FTKHVRIIEPGFVFIISYLSYLSLSEMLSLAILAI 312
 QY 279 FFCGIVMSHYTHWNTSESSRVTTKHAFAFATLSFIAETFLFYVGMMDALDIEKWEFASDRPG 338
 DB 313 TFCGICCCQYKVNISEQSAITVRYTMKMLASSAETIIFMFLGISAVNPFITW----- 366
 QY 339 KSIGISSILLGLVLIG--RAAFVFPFLSFLSNLTKKAPNEKITWROOVVIMWAGLMRGAVS 396
 DB 367 ---NTAFVLLTVFISYRAIGVLOTWLLNRYRMVQLEPI---DOVVLSTYGGGL-RGAVA 419
 QY 397 IALAYNKFTSRGHTOLHGNAI---MITSTIVVLFSTWVF--GMMTKPLIR--LLLPASGH 450
 DB 420 FALV-----VLLDGKVKKEKMLFVSTTIIVVFTVIFQGLTIKPLVQWLKVRSEH 470
 QY 451 PVTSEPPSPKSLH 463
 DB 471 ---REPRNLNEKLH 480

RESULT 5
 US-09-097-053-9
 Sequence 9, Application US/09097053
 Patent No. 6392025
 GENERAL INFORMATION:
 APPLICANT: Brant, Steven R.
 APPLICANT: Yun, Chris C.H.

APPLICANT: Donowitz, Mark
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human Nat/H+ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,053
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/677,734
FILING DATE: 10-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-00000
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-097-053-9

Query Match 17.7%; Score 482.5; DB 4; Length 834;
Best Local Similarity 31.4%; Pred. No. 3.6e-38;
Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;
Qy 48 VNESITALLIGCTGAVTMSFFFTISIAIAIFSRMNTIGTLDVG--FVSEDLFFIYLLPPIIFNAGFQVKKQF 105
Db 82 VPESALLIVGLVGGIV-----WAADHIASTLTPTVFFVLLPPIVLDAGYFMPNRLF 136
Qy 106 FRNFWTITLFGAVGTMSFFFTISIAIAIFSRMNTIGTLDVG--DPLATGAFSATDSVCT 163
Db 137 FGNLGTLLYAVGVVWNAATGSLYGVFLSGLMGDLQIGLLDFLLFGSLMAAVDPVAV 196
Qy 164 LOVLNO--DETFFLYSLVFGEGVNDATSIIVFNALQNFDLV---HIDAIVLKFGLNFFY 219
Db 197 LAVVEEVHVNVEFLIVFGESLLNDAVTVVLYNVFSEFVALGGDNVTGVCVKGVTSFFV 256
Qy 220 LFLSTFLG-VFAGLLSAYIIKKLYIGHSTDRVALMMLMAYLSYMLAELLDSLGLTV 278
Db 257 VSLGTLGVVVFALLS-LVTR--FTKHVRIEFGFVFIISYLSYLTSEMLSAIILAI 312
Qy 279 FFCGVMSHYTHNVHTSSRTTKHAFATLSFIATFTFLYVGMGDALDKWEFASDRPG 338
Db 313 TFCGTCCKYKANKISEQATTVRYTKMLASAEITIFMFLGISAVNPFITW----- 366
Qy 339 KSGISSTILGLVLIG--RAAFVPEPLSFLSNLTKKAPKEKITRQOVVWAGLMRGAVS 396
Db 367 ---NTAFVLLTFLVSYRAIGVVLQVTLNRYRMVQLEPI---DQVVLSTGGGL-RGAVA 419
Qy 397 IALYNKPTRSGHTQLHGNAI-----MITSTTVVLFSTWVF-GMWTKPLIR-LLLPASGH 450
Db 420 FALV-----VLLDGDVKVKERNLFVSTTIIIVFFTVIFQGLTIKPLVQWLKVRKSEH 470

Qy 451 PVTSEPPSPKSLH 463
Db 471 ---REPLNEKHLH 480
RESULT 6
US-09-097-053-10
Sequence 10, Application US/09097053
Patent No. 6392025
GENERAL INFORMATION:
APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human Nat/H+ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,053
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/677,734
FILING DATE: 10-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-00000
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-097-053-10
Query Match 17.7%; Score 482.5; DB 4; Length 834;
Best Local Similarity 31.4%; Pred. No. 3.6e-38;
Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;
Qy 48 VNESITALLIGCTGAVTMSFFFTISIAIAIFSRMNTIGTLDVG--FVSEDLFFIYLLPPIIFNAGFQVKKQF 105
Db 82 VPESALLIVGLVGGIV-----WAADHIASTLTPTVFFVLLPPIVLDAGYFMPNRLF 136
Qy 106 FRNFWTITLFGAVGTMSFFFTISIAIAIFSRMNTIGTLDVG--DPLATGAFSATDSVCT 163
Db 137 FGNLGTLLYAVGVVWNAATGSLYGVFLSGLMGDLQIGLLDFLLFGSLMAAVDPVAV 196
Qy 164 LOVLNO--DETFFLYSLVFGEGVNDATSIIVFNALQNFDLV---HIDAIVLKFGLNFFY 219
Db 197 LAVVEEVHVNVEFLIVFGESLLNDAVTVVLYNVFSEFVALGGDNVTGVCVKGVTSFFV 256
Qy 220 LFLSTFLG-VFAGLLSAYIIKKLYIGHSTDRVALMMLMAYLSYMLAELLDSLGLTV 278

Db 257 VSLGTLGVVFAFLLS--LVTR--FTKHVRRIEFGFVFIISYLTSEMLSLAILAI 312
 QY 279 FFCGIVMSHYTHNVTESSRVTTKHAFATLSFIAETFLFVYGVMDALDIEKWEFASDRPG 338
 Db 313 TFCGICCOQKYKANISEQASATVRYTMKMLASSAETIIFMFLGISAVNPFITWTW----- 366
 QY 339 KSIGISSITLGLVLIG--RAAFVFPFLSFLSLTKKAPNEKITWQQVVIWAGLMRGAVS 396
 Db 367 ---NTAFVLLTLVFSYVRAIGVLOTWLLNRYRMVQLEPI---DQVLSVGGI-RCAVA 419
 QY 397 ITALYNEKTRSGHQLHGNAI-----MTISTTVVLFSTWVF-GMWTKPLIR-LLLPASGH 450
 Db 420 FALV-----VLLDGDVKVKNLFSVTIIVVFTVIFQGLTIKPLVQWLKVRKSEH 470
 QY 451 PVTSPSPSKSLH 463
 Db 471 ---REPLNEKLH 480

RESULT 7
 US-08-677-734A-11
 ; Sequence 11, Application US/08677734A
 ; Patent No. 5871919
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 ; TITLE OF INVENTION: NHE3.
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/677,734A
 ; FILING DATE: 10-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fordis, Jean B.
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387.0043-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 831 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-677-734A-11

Query Match 17.7%; Score 480.5; DB 2; Length 831;
 Best Local Similarity 28.6%; Pred. No. 5.7e-38;
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;
 QY 22 VVSNLFVALLCACIV-LGHLLLEENRWNESITALIIGCTGVWILLMTKGKSSHL--FV 78
 Db 54 IIALWILVASLAKIVFHLSH--KVTSVVPESALLIVGLVGLGIV-----WAAADHIAFT 106

QY 79 FSEDLFFIYLLPIIFNAGQVKKKOFFRNMFTITLFGAVGTMTISFTTISIAAIAIFSRM 138
 Db 107 LTFTEFFIYLLPIVLDAGYFMRNLFEGNLGTLILYAYIGTWNATTCLSLYGVFLSG 166
 QY 139 NIGTLGVG--DFLAIGAIFSATDSVCTQLVNLQ--DETPFLYSLVFGGVVNDATSVLNF 195
 Db 167 LMGELKIGLDFLFGSLIAAADPVAVLAVFEVHVNEVLIIVFGESLLNDATVTVLYN 226
 QY 196 ALONFOLVHIDAAV---VLKFLGNFVFLSSTFLGV-FAGLLSAYLIKKLYIGRHSTDR 251
 Db 227 VFESVTVLGDATGVDCVKGIVSFFVSLGGTLGVGVIFAFLLS--LVTR--FTKHVRRI 282
 QY 252 EVALMMLMAYLSYLAELDLGILTVFCGIVMSHYTHNVTESSRVTTKHAFATLSFI 311
 Db 283 EPGFVVISYLSYLTSEMLSLAILAITFCGICCOQKYKANISEQASATVRYTMKMLASG 342
 QY 312 AETFLYVGMMDALDIEKWEFASDRPKSGISISILLGLVLIG--RAAFVFPFLSFLSNLT 369
 Db 343 AETIIFMFLGISAVDPVITW-----NTAFVLLTLVFSYVRAIGVLOTWLLNRY 393
 QY 370 KAPNEKITWQQVVIWAGLMRGAVSIALAYNKFTRSGHTQLHGNAMITSTITVVVLS 429
 Db 394 RMVQLETI---DQVMSYGGI-RCAVAYALV---VLLDEKVKKKNLFSVTTILVVFET 445
 QY 430 TMVEGMMTKPLIRLLLPASGHPVTSEPPSKSLH----SPLLTSMQSGDLESTNIVRPS 485
 Db 446 VIFQGLTIKPLVQWLKVRSE--QREPKLNEKLHGRAFDHLSAIEDISQIGHNVLRDK 503
 QY 486 SLRMLLTGKPTHVHYVYWRKFD-----DALMR 511
 Db 504 -----WSNEDRKFSLKVLMR 518

RESULT 8
 US-09-097-053-11
 ; Sequence 11, Application US/09097053
 ; Patent No. 6392025
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 ; TITLE OF INVENTION: NHE3.
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/097,053
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/677,734
 ; FILING DATE: 10-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fordis, Jean B.
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387.0043-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 831 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-097-053-11

Query Match 17.7%; Score 480.5; DB 4; Length 831;
 Best Local Similarity 28.6%; Pred. No. 5.7e-38;
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;
 QY 22 VVSNLFVALCACIV-IGHLEENRWNESITALIIGLCTGWILLMTKGKSSHL--FV 78
 DB 54 IIALWILVASLAKIVFHLSH--KVTSVVPESALLIVLGLVGIV-----WAADHIASFT 106
 QY 79 FSEDLEFYLLPPIIFNAGVKKQFFRNPMITLFGAVGTMTSFFITSTAAIAIFSRM 138
 DB 107 LPTLFFLYLLPPIIVLDAGYFMPNRLFFGNLTILLYAVIGTINNAATGSLXGVFLSG 166
 QY 139 NIGTLVVG--DFAIGAIFSATDSVCTLOVLNQ--DETFLYSLVFGVWVNDATSVILFN 195
 DB 167 LMGLKIGLLDFLFGSLIAAIVDPVAVLAVEEVHVNELFIVFEGESLLNDVTVLYN 226
 QY 196 ALQNFDLVHDAV---VLKFLGNFFYFLSSTFLGV--FAGLLSYIITKLYIGRHSTDR 251
 DB 227 VFESFVTLGGDAVGVDCVKIGIVSFVSVLGGTLGVIFAPLLS--LVTR--FTKHVRIL 282
 QY 252 EVALLMMLAYLSYMLAELLDLSGLITVFFCGIVMSHYTHNVTSSRVTTKHAFATLSFI 311
 DB 283 EPGFVVISYLSYLSLSEMLSLAILATFCIGICQKVKYKANISQSATTVYITMKMLASG 342
 QY 312 AETFLYVGMALDIEKWEFASDRPGKSGISISLLGLVLIG--RAAFVPLSFLSNLT 369
 DB 343 AETIFMPLGISAVDPVITWT-----NTAFVLLTLVFISVVRAGVVLQWILNRY 393
 QY 370 KKAPNEKITWQQVYVWAGLMRGAVSTALAYNKETRSCHTQHLGNALMITITIVVLFS 429
 DB 394 RWVQLETT---DQVMYSGGL--RGAVAYLV-----VLLDEKKVKRKNLFVSTTLIVVFT 445
 QY 430 TMVFGMTKPLIRLLPASGHVPTSESPSKSLH-----SPLITSQSGDLESTTNIVRPS 485
 DB 446 VIFQGLTIKPLVQMLVKRSE--QREPKNEKLHGRAPFDHLSAEDISGQIGHNYLRDK 503
 QY 486 SLRMLLKPHTVHYVWRKFD-----DALMR 511
 DB 504 -----WSNEDRKFLSKVLMR 518

RESULT 9
 US-09-134-001C-5576
 Sequence 5576, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 5576
 LENGTH: 683
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5576

Query Match 7.4%; Score 200.5; DB 4; Length 683;

Best Local Similarity 20.0%; Pred. No. 7.2e-11;
 Matches 86; Conservative 85; Mismatches 166; Indels 93; Gaps 17;
 QY 77 FVFSDELFFIYLLPPIIFNAGVKKQFFRNPMITLFGAVGTMTSFFITSTAAIAIFRS 136
 DB 53 FNFSELSFMTVLIAPLLFVEGVNVRVH--LRKYIKPVMMLGLVIT-----TVIGVGLFI 107
 QY 137 RMNIGTLDVGDFLAIGAIFSATDSVCTLOVLNQDETTP--FLYSLVFGVWVNDATSV--- 192
 DB 108 HWIWPFLPIGAFAAAILCPDVAVAOAITKGKVLPGKSWTILLEGESLNDAAGLISPK 167
 QY 193 -----LFNALQNFDLVHIDAADVFLKFLGNFFFLSSTFLGVFAGLZLSAYII 239
 DB 168 IAVGVLLITGTTESIFDAIQOFLIASIGGAIV-----GLIIGMALVRFRL 210
 QY 240 KKLYICRSTREVALMMLMAYLSYMLAELLDLSGLITVFFCGIVMSHYTHNVTSSRV 299
 DB 211 TLMRGIEINMFTPIQLTTPVTYLIABLPHASGIIAAVAVAGLV-----HCFERDRIA 264
 QY 300 TTK-----HAFATLSFIATFTFLYVGMALDIEKWEFASDRPGKSGISISLLGLV 351
 DB 265 QTRTQLOMSYNTWSILGYVLNGFVFSILGLFVPEVIV--KIITKPHNLLFVITL--- 320
 QY 352 LIGRAAFV-----PLSFLS-----NLTKAPNEKITWQQVYVWAGLM-----R 392
 DB 321 LVALAVYLFRVWVYVLYPYFVLSVPFQKMSKNDKDKVTSKPKRSYALIMTLGCVH 380
 QY 393 GAVSTALAYN--KETRSGH--TQHLGNALMITITIVVLTSTVFGVWMTKPLIRLLPASGH 450
 DB 381 GTISLAIATLTPYLLANHETFAIRNDLLFIASGMVIL--SLIAQVILPLV----- 429
 QY 451 PVTSEPPSPK 460
 DB 430 ---TPDSPE 435

RESULT 10
 US-09-014-969-11
 Sequence 11, Application US/09014969
 Patent No. 5965397
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: McCoy, John M.
 APPLICANT: Lavallie, Edward R.
 APPLICANT: Racie, Lisa A.
 APPLICANT: Merberg, David
 APPLICANT: Treacy, Maurice
 APPLICANT: Spaulding, Vikki
 APPLICANT: Agostino, Michael J.
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/014,969
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sprunger, Suzanne A.
 REGISTRATION NUMBER: 41,323
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-014-969-11

Query Match 4.8%; Score 130.5; DB 2; Length 635;
Best Local Similarity 19.1%; Pred. No. 0.00041;
Matches 118; Conservative 86; Mismatches 206; Indels 209; Gaps 25;

QY 3 MEVAARLALGALYTTSDYA-----SVSINLFVALLCACIVLGHLLLENRWVNESITALI 56
DB 1 MSVGSTSAPLSPSTSGTSGVSTSTFIMDYVVFVLLLVLSLAIGLYHACRGWRTVGEELL 60
QY 57 IG---LCTGVVILLMTKGS-----SHLFVSEDLFFI-----YLLPPIIFNAG 97
DB 61 MADRKMGCLPVALLSLATFQSAVALTRVPSIYREGTQYWFRLCCYFLGLLIPAHIF--- 117
QY 98 FOVKKKQFRNPMITLFGAVGTMISPTTISIAATAIFSRNMGITDVGDFLAIGAIPSA 157
DB 118 -----IPVEYRHL--TSAYEYLELR--FNK 139
QY 158 TDSVCTQLVQNDPFFLYSLVFGVGVNDATSIIVLFNALONFDLVHIDAADVLFKLGNF 217
DB 140 TVRVC-----GVTFTFQMVYMGVLYAPSLAL-NAVTFD----- 175
QY 218 FYLFSSSTFLGVFAGLLSAYIKKLYIGRHSVDREVALMMLMAYLSYMLAEILDISGILT 277
DB 176 --LWLSVALRIVCTVYTAGLKAIV---TDVFTLVMLGOLAVIIVGSARKVGLGR 230
QY 278 VFFCGIVMSHYTHNVNTESSRVT-----TKHAFATLSFIATFTFLFYVGMDDALDIE 328
DB 231 V-----WAVASQHRIGSGFELDPDPFVRHTFTWTLAFGGVFMMLSLYGVNAQOV 279
QY 329 KWEEASDRPKSGISGLS-----STLLGLVLIG-----RAAFVEP 361
DB 280 R--YUSSRTEKAUVLSVCYAVFPFQVQVLCVGLGLGVFAFYOEYPMISQQAAPDFV 337
QY 362 LSFLSNLTKKAPNEKITRQOVVIVWAGLIRGAVS--IALAYNKFTRSGHTQL----- 412
DB 338 LYFVNDLLKGLPG-----LPGLFIACLFSGSLSTISSAFNSLATVMTMEDLIRPWFPEF 390
QY 413 -HGNAMITSTT-----VVLFTWVFGMMTKPLIRLLLPASGHPV 452
DB 391 SEARAIMLSRGLAFGYGLLCLGMAYISSQMGFVLQAAISIFQVGGPGLLGLFCIGMFFPC 450
QY 453 TSEPSPKSLHSP-----LTSM-----QGSLESTTN--IVRPSLSRLM 490
DB 451 ANPPGAVGLLAGLWAFWIFIGISIVTSMGFSMPSPSGSFSFLPTNLVTATVTTMLPL 510
QY 491 LT--KPT-----HTVHYW 502
DB 511 TTFSEKPTGLQREYSLSYLW 529

RESULT 11

US-09-134-001C-4425
; Sequence 4425, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4425
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4425

Query Match 4.6%; Score 124.5; DB 4; Length 605;
Best Local Similarity 22.9%; Pred. No. 0.0015;
Matches 106; Conservative 69; Mismatches 190; Indels 97; Gaps 24;

QY 22 VVSINLFVALLCACIVLGHLLLENRWVNESITALIIGLCTGVVILLMTKGSKSHLFVSE 81
DB 18 MLTIVLFLAL--GIFSQWLASRIKWPFSIVVMA-IVGLLVGPIFGLANKEALGPEAFSS 73
QY 82 DLFFIYLLPPIIFNAGQVKKKQOFFRNFMTITLFGAVGTMISPTTIS-----IAAIAIF 135
DB 74 ---IVSLAVAAIL---FEGSSNLDRE---LKGISKAVIRIITIGAGTAWILGAILAH 122
QY 136 SRMNIPTDVGDFLAIGAIFSATDSVCTQLVQNDPFFLYSLVFGVGVNDATSIIVL 193
DB 123 VTMMF-PLSIS--FVIGGLFLITGPTVIQIQLLQAKVRNVDVLRWESIIIDPGLPIA 179
QY 194 FNALQNFDELVIDAAVYLVKFLGNFFYFLSSTFLGVFAGLLSAYIIKKLYIGRHSSTREV 253
DB 180 LTAFYVVFQIFEEGIGLVVIL--FILKLAAILIGFGAFLFNWLI-----SQDKIP 229
QY 254 ALMMLMAYLSYMLA-----ELDLGILVFGCGIVMSHYTHNVNTESSRVTTKHAFAT 307
DB 230 QSLMPTQLVFIILTFSEIDELSESGLLAVTFGLMMARKKRHDLFKE---SDHFIDN 286
QY 308 LSFTAETFLFYVGMQD---ALDIEKWERASDRPKSGISGISTLLGLVLIGRAAFVEPL 362
DB 287 ASSILVSTFILLITSSITKDVLLNLSWLQ-----ILFSLVMI---VLVRPI 330
QY 363 S-FLSNLTKKAPNEKITRQOVVIVWAGLM--RGAVSIALAYNKFTRSGHTQLHGNAM- 418
DB 331 SVLLSTL---GTEITKKERAVV---ALMAPRGIVVLTVA-----QFESSLFMD 372
QY 419 -----ITS-TTIVVLFSTWVFGMMTKPLIRLLLPASGHP 451
DB 373 DKIPMAQYITPVTGVLVITVVIYGFGTPLSLKFLGVASTEP 414

RESULT 12

US-09-134-001C-5655
; Sequence 5655, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5655
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5655

Query Match 4.4%; Score 118.5; DB 4; Length 800;
Best Local Similarity 21.3%; Pred. No. 0.0085;
Matches 101; Conservative 71; Mismatches 173; Indels 129; Gaps 22;
QY 57 IGLCTGVVILLMTKG-----KSSHLFVSEDL--FFIYLLPPIIFNAGFQVKKKOFFRNF 110

Db 79 LSLFGLIILSIGVGFYATQYLSHSTDNLPRFIYLLLFMFSGMIGVIA-----NNTI 133
QY 111 TITFGAVGTMTISFTTIS-----IAATAIFSRMNIIGTLDVGDGLAIGAIFSATDSV 161
Db 134 LMVFWELTSSISSULLISYWNNGESQLGAIQSPMITVFGGLALLTGFIILYIITGTNTI 193
QY 162 CTLOVQNODET-----PFLYSLVFGEVGVNDATSVLNFALONFDL----- 202
Db 194 ---TDILNORNAISRHPLFIPIMILMLLG-----AFTKSAQFPFHILWLPKMAAP 240
QY 203 ---VHIDAADVVLKFLGNFFFLSTSTFLGVFAGLLSAVIKKLYKLGHRSTDRVALMML 258
Db 241 TPVSAYLHSAFMVK--AGIFILFRFETPL-----GLSNVYIIVTFVG-----LIT 284
QY 259 MAYLSYMLAEILLDSGIL---TVFPCGVMS-----HYTHNVTPESSRVTTKHAFATLS 309
Db 285 MLFGSLTALROYLDKILAYSTISOLGIMTVMVGLGGGYAQHTSDLSKFIYLVLFAGLF 344
QY 310 FIATETFL---LYVGMALDIEKWEFASDRPKSGISG-----ISSILLGLVLIG-- 354
Db 345 HLMHNAVFKCALFGVGVGIIDHE-----SGTRDIRLLNGMRKVFPKMHIVMLLAALSMAAGVP 400
QY 355 -RAAFVPLSFLSNLTKKAPNEKITRQOVVIMWAGLMRGAVSIALA-----YN 402
Db 401 FLNGFLSKEMFLDSLTKANELDQYGFVLTFVLISGVIASILTFYALYMIKETFWGNYN 460
QY 403 --KTRSHGTOHNG-----NAIMTSTITVFLSTWVFGMMTKPLIRLLPAS 448
Db 461 IEKPKK---QIHEPWLFLSPLAVILMLLPIVFFPNVFGNF-----VILPAT 505

RESULT 13
US-09-134-001C-3487
; Sequence 3487, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3487
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3487

Query Match 4.2%; Score 114; DB 4; Length 477;
Best Local Similarity 20.5%; Pred. No. 0.011;
Matches 103; Conservative 84; Mismatches 189; Indels 126; Gaps 25;

QY 15 TTSYASVWSINL---FVALL-----CACIVLGHLEEN--RWYNESITA--LIIGL 59
Db 12 TTSRNVAVTVMILSAFVSMLNOTILNTALPAIKGLNITETTAAQL---ITGFMLVNGI 68
QY 60 CTGVVILMTKGSLSHLFVSEDLFF-----IYLLPPII--FNAGFOVKKKQ 104
Db 69 MIPLTAFMDKYSTRHYLFESMAIFLGISVAAPSPFTILMISRIIOAIGALLPLMQ 128
QY 105 FFRNFMITLFGAVGTMTISFTTISIAAIAIFSRMNIIGTLDVGDGL-----AI 151
Db 129 ----FTVETLFPAAEQ---RCFAMGLAGVVVQSAPAIQTLTGLFVDLFSRMPFYLVSAL 181
QY 152 GAI-----FSATDSVCTLOVQNODETPFLYSLVFGEVGVNDATSVLNFALONFDLVI 205
Db 182 AAVAFILGFFGVENNTKTQIV-LDKISVYVS-TFGGLI-----LFAFSSVSTFGITSL 234

QY 206 DAAVVLKELGNFFYFLSSTFLGVFAGLLSAVIKK-----LYIGHRSTDEV 253
Db 235 -PVIATVEVLGIAIIIFITRQLKHLPLNMRVFNKNKFTLSAVSSMLVYITMVS----- 288
QY 254 ALMMLMAYLSYMLAEILLDSGILTVFFCGIVMSHVTWNVTPESSRVTTKHAFATL----- 308
Db 289 PALLPIYIOTGLGQSALLSGV--VVLPGAVINGLT--MVYTGKIFDKHGKVLVPGF 343
QY 309 -SFIAETFLVGVGMALDIEKWEFASDRPKSGISGISTLLGLVLIGRAAFVPLSFLS- 366
Db 344 ILLISMTFLYSEF-----TTGPPYWFVILVYTIIRMLALGLLVMPLNTVGL 388
QY 367 NLTKAPNEKITRQOVVIMWAGLMRGAVSI---ALAYNKFTRSQHTQ-----LH 413
Db 389 NALESDDVSHGTAIINSLRIIAGAMGTAVSVTILSIVAKQYTAHSTKSKMLTOEATVH 448
QY 414 G--NAIMTSTITVFLSTWVVF 433
Db 449 GIDVAFIETVLLIIGFITALF 470

RESULT 14
US-09-213-053-2
; Sequence 2, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: PRT
; ORGANISM: Canine herpesvirus
US-09-213-053-2

Query Match 4.2%; Score 113; DB 4; Length 1394;
Best Local Similarity 21.6%; Pred. No. 0.067;
Matches 119; Conservative 87; Mismatches 206; Indels 140; Gaps 27;

QY 10 LGALYTTSDYASVVSINLFLVALLCACIVLGHLEENRWYNESITAIIIGLCTGV----- 64
Db 454 LPCMYVTT--KSLLCIGLOAGILTALIILQIL-----TESFVCSIIILATVLIIFTLSK 505
QY 65 ILLMTKCKSSHLFVSEDLF-----FIYLLPPIIFNAGFOVKKKQFFRNEMTITLF 115
Db 506 ISITSFKISISICRISQSFVTTAAFCWGFDMILNPIA-----IKILI 549
QY 116 GAVGTMISFTTISAAIAIFSRMNI-----GTLDVGDFLAIGATFSATDSVCTLOV 166
Db 550 ----LSLSFLTCTIKTHIFLISILNGSGSHVKGSLVTLFGILGVG-----LNV 599
QY 167 LNODETPFLYSLVFGEVGVNDATSVLNFALONFDLHIDAADVVLKFLGNFFYFLSSTF 226
Db 600 IK-----TEILIGFGI---ALCIILSNT--NEGLVIRDTFCYVR--IGRY---KLMRTF 642
QY 227 LGVPAGLLSAVIKKLYKLGHRST--DREV-ALMMLMAYLSYMLAEILLDSGILTFVFCGI 283
Db 643 TDGLHG--ASYSEDEETSQYSEIHERKISSFQIYKYPSMIISILGFMILTIAIWLNV 700
QY 284 VMHSYTHWNVTESRVTTKHAFAT---LSFAETFLVYVGMALDIEKWEFASDRPKGS 340
Db 701 YLKNLKFH-----SPFTLVISFVGHCLAFVFPFNKIKICRI----- 740

QY 195 NALONFDLVHDAVWLKFLGNFFYLSSTFLGVFAGLLSAYIITKLYIGRHSTDEVA 254
Db 195 NAIQSFDLTHLNEAARQFLGNFFYLSSTFLGVATGLISAYVVKLYIGRHSTDEVA 254
QY 255 LMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRVTTKHAFATLSFAET 314
Db 255 LMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRVTTKHAFATLSFAET 314
QY 315 FLFLYVGMADLDIEKWEPFASDRPGKSGISGILGLVIGRAAFVFLSFLSNLTKKAPN 374
Db 315 FLFLYVGMADLDIEKWEPFASDRPGKSGISGILGLVIGRAAFVFLSFLSNLTKKAPN 374
QY 375 EKITWROQVVIWAGLMRGAVSALAYNKETRSCHTOLHGNAMITSTITWVLFSTWVFG 434
Db 375 EKISIKQOVVIWAGLMRGAVSALAYNKETRSCHTOLHGNAMITSTITWVLFSTWVFG 434
QY 435 MMTKPLIRLLP-----ASGHPTVSEPSKSLHSPLLTSMQSDLE--STNIVRPSS 486
Db 435 MMTKPLIRLLP-----ASGHPTVSEPSKSLHSPLLTSMQSDLE--STNIVRPSS 486
QY 487 LRMLLTKPHTVHYWKRFDALMRPMFGGRGFVPFSPGSPTEQS 531
Db 487 LRMLLTKPHTVHYWKRFDALMRPMFGGRGFVPFSPGSPTEQS 531
QY 495 LRGFLMRPRTVHYWKRFDALMRPMFGGRGFVPFSPGSPTEQS 539
Db 495 LRGFLMRPRTVHYWKRFDALMRPMFGGRGFVPFSPGSPTEQS 539

RESULT 2

US-09-834-998A-1

; Sequence 1, Application US/09834998A

; Patent No. US20020178464A1

; GENERAL INFORMATION:

; APPLICANT: Gaxiola, Roberto A.

; APPLICANT: Fink, Gerald R.

; APPLICANT: Alper, Seth L.

; TITLE OF INVENTION: Proton Transporters And Uses In Plants

; FILE REFERENCE: 0399.2004-002

; CURRENT APPLICATION NUMBER: US/09/834,998A

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 09/644,039

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: US 60/164,808

; PRIOR FILING DATE: 1999-11-10

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Arabidopsis - AtNhx1

US-09-834-998A-1

Query Match

Best Local Similarity 74.3%; Score 2023.5; DB 9; Length 538;

Matches 389; Conservative 60; Mismatches 79; Indels 3; Gaps 2;

QY 3 MEVAAARLGALYTTSDYASVVSINLFLVALLCACIVLGHLLLEENRWANESITALIIGLC 62
Db 3 LGLSTMLEKTEALF-ASDHASVVSINLFLVALLCACIVLGHLLLEENRWANESITALIIGLC 62
QY 61 TGVVILLMTKGSLSHLFVSEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGTMI 122
Db 61 TGVVILLMTKGSLSHLFVSEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGTMI 122
QY 123 SFTTISIAAIAIFSRMNTGTLVDGFLAIGAFSATSVCVTLQVNDQETPLLYSLVGE 182
Db 123 SFTTISIAAIAIFSRMNTGTLVDGFLAIGAFSATSVCVTLQVNDQETPLLYSLVGE 182
QY 183 GYVNDATSVIFNALQNFDLVHDAVWLKFLGNFFYLSSTFLGVFAGLLSAYIITK 242
Db 183 GYVNDATSVIFNALQNFDLVHDAVWLKFLGNFFYLSSTFLGVFAGLLSAYIITK 242
QY 243 YIGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRVTTK 302
Db 243 YIGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRVTTK 302

Db 241 YFGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRVTTK 300
QY 303 HAFATLSFAETFLFLYVGMADLDIEKWEPFASDRPGKSGISGILGLVIGRAAFVFLP 362
Db 303 HAFATLSFAETFLFLYVGMADLDIEKWEPFASDRPGKSGISGILGLVIGRAAFVFLP 362
QY 363 SFLSNLTKKAPNEKITWROQVVIWAGLMRGAVSALAYNKETRSCHTOLHGNAMITST 422
Db 363 SFLSNLTKKAPNEKITWROQVVIWAGLMRGAVSALAYNKETRSCHTOLHGNAMITST 422
QY 423 ITVVLFTWVFGMMTKPLIRLLPASGHPVT--SEPSPKSLHSPLLTSMQSDLESTN 480
Db 423 ITVVLFTWVFGMMTKPLIRLLPASGHPVT--SEPSPKSLHSPLLTSMQSDLESTN 480
QY 481 IVPSSIRMLLTTPHTVHYWKRFDALMRPMFGGRGFVPFSPGSPTEQS 531
Db 481 IVPSSIRMLLTTPHTVHYWKRFDALMRPMFGGRGFVPFSPGSPTEQS 531

RESULT 3

US-10-155-535-4

; Sequence 4, Application US/10155535

; Publication No. US20030046729A1

; GENERAL INFORMATION:

; APPLICANT: Blumwald, Eduardo

; APPLICANT: Apse, Maris

; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY

; TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPOETERS

; FILE REFERENCE: 529152000720

; CURRENT APPLICATION NUMBER: US/10/155,535

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: 09/271,584

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,474

; PRIOR FILING DATE: 1998-03-18

; PRIOR APPLICATION NUMBER: 60/116,111

; PRIOR FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 552

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-155-535-4

Query Match

Best Local Similarity 70.9%; Score 1931; DB 9; Length 552;

Matches 377; Conservative 67; Mismatches 78; Indels 20; Gaps 4;

QY 1 MGEVAAARLGALYTTSDYASVVSINLFLVALLCACIVLGHLLLEENRWANESITALIIGLC 60
Db 1 MGEVAAARLGALYTTSDYASVVSINLFLVALLCACIVLGHLLLEENRWANESITALIIGLC 60
QY 61 TGVVILLMTKGSLSHLFVSEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGT 120
Db 61 TGVVILLMTKGSLSHLFVSEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGT 120
QY 121 MISFETISIAAIAIFSRMNTGTLVDGFLAIGAFSATSVCVTLQVNDQETPLLYSLV 180
Db 121 MISFETISIAAIAIFSRMNTGTLVDGFLAIGAFSATSVCVTLQVNDQETPLLYSLV 180
QY 181 GYVNDATSVIFNALQNFDLVHDAVWLKFLGNFFYLSSTFLGVFAGLLSAYIITK 240
Db 181 GYVNDATSVIFNALQNFDLVHDAVWLKFLGNFFYLSSTFLGVFAGLLSAYIITK 240
QY 241 KLYIGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRV 300
Db 241 KLYIGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRV 300
QY 301 TKHAFATLSFAETFLFLYVGMADLDIEKWEPFASDRPGKSGISGILGLVIGRAAFV 360
Db 301 TKHAFATLSFAETFLFLYVGMADLDIEKWEPFASDRPGKSGISGILGLVIGRAAFV 360
QY 362 YIGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRV 420
Db 362 YIGRHSTDEVALMMLAYLSYMLAELDLGLTVPFCGIVMSHYTHWNTVTESSRV 420

Query Match	19.98;	Score 541.5;	DB 10;	Length 509;
Best Local Similarity	30.88;	Pred. No. 1.5e-39;		
Matches 149;	Conservative 81;	Mismatches 173;	Indels 81;	Gaps 14;

QY	23	VSINLFVALLCACIVLGHLEEN--RWNVESITALLIGCTGWILL--	---MTKGGKSHL- 76
	: : :	: : : : : : :	
Db	19	VALLTFIILLTTLITLWPKRRVRELHETGLAMTYGLIVGYLPATSGRDKSL 78	
	: : :	: : : : : : :	
QY	77	-----FVSEDLDFEIVLLPPI 92	
	: : :	: : :	
Db	79	CTQEDRAFSTLLVNVSGFFPYTLKGELSPGKINSVEQNDMLRKVTDFEVEFNILLPPI 138	
	: : :	: : :	
QY	93	IFNAGQVKKKQFFRNFWMTITLFGAVGTMTISFTTISIAATAIFSRMNI--GTLD--	--VGD 147

Query Match 19.6%; Score 533; DB 9; Length 633;
Best Local Similarity 26.2%; Pred. No. 1.2e-38;
Matches 153: Conservative 127; Mismatches 100; Indels 1

Qy	16	TSDYASVVSNLNFVALLCACIVGLHLEEN--RWYNESITALIIGCTGVILLMTKGS	73
Db	55	TEEMFSSWALFIMLLLIISALWSYYLTQKRIIRAVHTVLSIFYGMVIGLIIRMSPGHY	114
Qy	74	SHLPVESEDLFFIYLLPPIIFNAGQVKKQFFRNFWITLFCAGVTMISFFTTISATAA	133
Db	115	QDTVTFNSSYFVNLLPPIILNSGYELNQVNFNNMLSLIFAIPOGTFISAVVIGI--ILY	173
Qy	134	IFSRMNIITLDV--GDFALGAIFASDTSVCTQLVNQDET--PFLYSLVFEGGVNDAS	190
Db	174	IWTFGLGESIDISFADAMSGVATLSATDPVTILSIFNAYKVDPKLTIIFGESLLNDAS	233
Qy	191	IVLFNALQNFDLVHIDAENVLKLFGNFFYFLSSTFLGVFAGLLSAYIIKKLYIGHSTD	250
Db	234	IVMFETCKQKHGPOPATFSSVFEGAGLFLMTFSVLLIGVLIGILVALLKHTHRRY--PQ	292
Qy	251	REVALMMLMAYLSYMLAELDLDSGLITVFCGIVMSHYTHWNTSESRVTTKHAFTUSF	310
Db	293	IESCLLLIAYESYFFSNGCHMSGVSLGFCGILTKHAYIYNMRSRSQITIKYIFOLLAR	352
Qy	311	IATFTFLYVGMDAL--DIEKWEFASDRPGKSGISISLGL---VLIGRAAFVPEPLS--	363
Db	353	LSENFYIYGLGLFTEVE-----LYYKPLLIIVAASITCVARWCAVPFLSQF	400
Qy	364	-----FLSNITTK---APNEKITRWQOVITWAGLMRGAVSIALAYN-----KF	404
Db	401	VNWIYRVKTIIRMSGITGENISVPDE--IPYQOMMTFWAGL--RGAVGVALALGIOGEYKF	458
Qy	405	TRSGHTQLHGNAIMTITSTIVLFSFTWVGMMTKPLIRLLLPASGHPIVTSPESSPK--SL	462
Db	459	T-----LLATVLVVVVLTIIIFGGTAGMLEVINIKTG--CISEEDTSDEDFDI	505
Qy	463	HSP--LLTSSMOGSDLE-----STP-----	479
Db	506	EAPRAINLLNGSSIQTDLGPYSDNNSPDISIDQFAVSSNNKNLPNMISTGGTFCGLNET	565
Qy	480	-----NIVRPS-----SLRMLLTKPHTVHYWRKFDALMRPMF	514
Db	566	ENTSPNPARSSMDKRLNRKLGITIFNSDSOWFONFDEOVLKPVF	609

RESULT 11

US-10-217-096-6
; Sequence 6, Application US/10217096
; Publication No. US20030044933A1

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; APPLICANT: Curtis, Rory A.J., Ferreira, Holly M.
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
; FILE REFERENCE: MP101-147PIRM
; FILE REFERENCE: MP101-147PIRM

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; CURRENT APPLICATION NUMBER: US/10/217,096
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-096-6

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Query Match 17.8%; Score 485; DB 9; Length 896;
Best Local Similarity 29.9%; Pred.No. 3e-34;
Matches 155; Conservative 93; Mismatches 190; Indels,

QY 22 VVSINLFVALLCACIVLGHLLER-NRWVNESITALIIGLCTGVVILLMTCKKSSHLFVS 80

Db 49 LVALLMILVASLAK--IVFHLRSKVTSLVPESCLLILGLVLGGIVICAVAKAEYQL---E 103
Qy 81 EDLEFVILPPIIFNAGQVKKOFFRNFMTITLFGAVGTMISFFFTISIA-----AIAI 134
Db 104 PGTFFLFLPPIVLDGSGVFPNRLFFDNLGAILTYAVVGTLWNAFTTGAALWGLQOAGLV 163
Qy 135 FSRNIGTLDVGDPLATGAIFSATDSVCTLOVLNQ-----DETPFLYSLVFGGVVNDATSI 191
Db 164 APRVQAGLL---DFLLFGLSISAYDPVAVLAVFEEHVHNET--LFIIVFGESLLNDAVTV 218
Qy 192 VLENALONF---DLVHIDAADVAVLFGNFFVFLSSTFLG-VPAGL--LSAIYIKKLYIG 245
Db 219 VLYKCNSEFVEMGSAVQATDYLGKVASLFWVSLGGAAVGLVPFALLALTRFTKRVRI- 277
Qy 246 RHSTDREVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMSHYTHVNVNTESSRVTTHKAF 305
Db 278 -----IEPLLVFLAYAAAYLTAEMASLSAILAVTMCGLGCKKYEANISHKSRVTVKYTM 332
Qy 306 ATLSFIATFTFLYVGMADLDIEKWEFASDRPGKSGISSTLLG---LVLIGRAAFVFPPL 362
Db 333 KTLASCAETVIFMLLIGISAYDSSKAWD-----SGLVLGTLPILFFRALGVLVQ 382
Qy 363 SFLSNLTKKAPNEKITRQOVVIMWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTST 422
Db 383 TWLVNQFLVPLDKI---DQVMSYGG-RCAVAFALV---ILLDRTKVPADYEVATT 434
Qy 423 ITVLFSTVMFGMMTKPLIR-LLLPASGHPVTSEPPSKLSHSPLLTSMOGSDLESTNI 481
Db 435 IVWFVFTVVOGLTIKPLVKLVKVRSEH---HKPTLNQELHENTFDHI-----LAAVEDV 487
Qy 482 VRPSSRLMLTKPHTVHYV---WRKED-----DALMR 511
Db 488 V-----GHHGYHWDRWEQFDKYLSQLMLR 514

RESULT 12
US-09-824-734-3
; Sequence 3, Application US/09824734
; Patent No. US20020083485A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, JIAN-KANG
; APPLICANT: SHI, HUAZHONG
; APPLICANT: ISHITANI, MANABU
; APPLICANT: STEVENSON, BECKY
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
; FILE REFERENCE: 205644US20
; CURRENT APPLICATION NUMBER: US/09/824,734
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/194,648
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-09-824-734-3

Query Match 17.6%; Score 478; DB 10; Length 822;
Best Local Similarity 28.7%; Pred. No. 1.le-33;
Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;
Qy 18 DYASV---VSINLFVALLCACIVLGHLEE-NRWVNESITALIIGLTCGVVILLTKGKS 73
Db 99 DVLHVTPEISLWILLACIMKIGFHVPTISSIVPESCLLIVGLLVGGGLI---KGV 154
Qy 74 SHLFVPESEDLFFYLLPPIIFNAGQVKKOFFRNFMTITLFGAVGTMISFFFTIS--IAA 131
Db 155 ETPFPFLOSDFVFLPPIILDAGYFLPLRQFTENLGLTILFAVGTLWNAFFLGLLYA 214
Qy 132 IAIFSRMNTGTLVDGDFLAIGAIFSATDSVCTLOVLNODE--TPFLYSLVFGGVVNDATSI 190

Db 215 VCLVGEQINNIGLDTLLFGSIIISAVDPVAVVAVFEEIHINELLHLVFGESLLNDAVT 274
Qy 191 IVLENALQ---NPDLVHIDAADVAVLFGNFFVFLSSTFLGVPAGLLSYIYIKKLYIGRH 247
Db 275 VVLYHLFEFANYSIGI-SDIFLGLF-SFFVVALGGVGVVGVVIAAFTSR---FTSH 329
Qy 248 STDREVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMSHYTHVNVNTESSRVTTHKAFAT 307
Db 330 IRVIEPLFVFLYSYMLAEILLDLSGILTVFCGIVMSHYTHVNVNTESSRVTTHKAFAT 389
Qy 308 LSFIAETFLYVGMADLDIEKWEFASDRPGKSGISSTLLGILGLVIGRAAFVFPPLS 366
Db 390 WSSVSETLFIPLFGVSTVAGSHQWNV-----TFVISTLL--FCLIARVLVGLVLTWFI 440
Qy 367 NLTKKAPNEKITRQOVVIMWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMTSTITVV 426
Db 441 N---KFRIVKLTPKDQFIAYGGL-RCATAFSIGY--LMDKKRHPMCD--LFTALITVI 492
Qy 427 LFTVMVFGMMTKPLIRLLLPASGHPVTSEPPSKLSHSPLLTSMOGSDLESTTNIVRPS 486
Db 493 FTFVFGQMTIRPLVDLL-----AVKKQETKRSINEEHTQFLDHLTLGIEDIC---- 542
Qy 487 LRMLTKPHTVHYVYWRKFPDDALMR 511
Db 543 -----GHYGHHWK---DKLNR 556

RESULT 13
US-09-800-729-215
; Sequence 215, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 215
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-215

Query Match 11.5%; Score 314; DB 10; Length 370;
Best Local Similarity 29.8%; Pred. No. 9.8e-20;
Matches 88; Conservative 54; Mismatches 117; Indels 36; Gaps 10;
Qy 227 LGVFAGLLSAYIIR-KLYIGRHSTDRVALMMLMAYLSYMLAEILLDLSGLTVFCGIV 284
Db 1 MGAVTGVVLTAVTKTKLHC---FPLLETFLFLLMSTFLLAACGCTGVVAVLFCGIT 57
Qy 285 MSHYTHVNVNTESSRVTTHKAFATLSFIATFTFLYVGMADLDIEKWEFASDRPGKSGIS 344
Db 58 QAHTYNNLSVESRSRRTKQLEVLHFLAENFIFSYMGLALFTFOKHVS---PIFIIG-- 112
Qy 345 SILGLVLIGRAAFVFPPLSFLSNLTKKAPNEKITRQOVVIMWAGLMRGAVSIALAYNKF 404
Db 113 --AFVAIFLGRAAHYPLSPFLNLGRR---HKIGNFQHMFMFSG-L-RCAMAFALAIR-- 164
Qy 405 TRSGHTQLHGNAIMTSTITVFLSTVFGMMTKPLIRLLLPASGHPVTSEPPSKLSH 464
Db 165 ----DTASYARQMFTTLLVFFTVIIGGTTPLMSWL-----NIRVGDPODDPPNN 216
Qy 465 PLLTSMOGSDLESTTNIVRPSSRLMLTKPHT--VHYVWRKFDALMRPMEGGRG 518
Db 217 DSFVQLQDGG-----PDSARCNRTKQESAWIFRLWYFDHNYLKPILTHSG 262

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model
Run on: March 26, 2003, 18:50:39 ; Search time 21 Seconds
(without alignments)
2449,139 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAAALGALYTTSDYA.....GRGFVPFSPGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1698.5	62.4	457	2 T01804	Na+/H+-exchanging
2	567.5	20.8	629	2 T22848	hypothetical prote
3	564.5	20.7	703	2 T26529	hypothetical prote
4	552	20.3	569	2 T37706	probable sodium/hy
5	533	19.6	633	2 S69734	hypothetical prote
6	492	18.1	832	2 A40205	Na+/H+-exchanging
7	485	17.8	809	2 A46747	Na+/H+-exchanging
8	481	17.7	816	2 S16328	Na+/H+-exchanging
9	480.5	17.7	831	2 B40204	Na+/H+-exchanging
10	479	17.6	813	2 A46748	Na+/H+-exchanging
11	478	17.6	822	2 S30198	Na+/H+-exchanging
12	476	17.5	818	2 A48858	Na+/H+-exchanging
13	474	17.4	815	2 I57487	Na+/H+-exchanging
14	472	17.3	759	2 A46188	CAMP-activated Na+
15	463	17.0	820	2 A40204	Na+/H+-exchanging
16	460.5	16.9	698	2 A57644	Na+/H+-exchanging
17	456	16.8	717	2 C40204	Na+/H+-exchanging
18	427	15.7	478	2 T18746	Na+/H+-exchanging
19	397	14.6	375	2 B40205	Na+/H+-exchanging
20	396.5	14.6	634	2 T33528	hypothetical prote
21	395	14.5	651	2 T31869	hypothetical prote
22	394.5	14.5	602	2 H88215	protein B0495.4 [1
23	393	14.4	798	2 T23539	hypothetical prote
24	385.5	14.2	660	2 T28016	hypothetical prote
25	349.5	12.8	609	2 S30910	Na+/H+-exchanging
26	343	12.6	520	2 AD2383	Na+/H+-exchanging
27	316	11.6	527	1 S75063	Na+/H+-exchanging
28	312	11.5	531	2 D96827	protein F20B17.4 [
29	290	10.7	494	1 F69355	Na+/H+ antiporter

ALIGNMENTS

RESULT 1

T01804

Na+/H+-exchanging protein 3 homolog A_TM021B04.4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Oct-1999
C:Accession: T01804
R:Dante, M.; Wamsley, P.; Gibson, A.
Submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana TM021B04.
A:Reference number: Z14440
A:Accession: T01804
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-457 <DAN>
A:Cross-references: EMBL:AF007271; NID:g2191181; PID:g2191184; GSPDB:GN00063; ATSP:A-
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP:A_TM021B04.4
A:Map position: 5
A:Introns: 55/3; 95/2; 128/1; 148/1; 163/3; 240/3; 256/2; 286/3; 320/2; 400/3; 421/3

30	279.5	10.3	527	2 AE2932	Na+/H+ antiporter
31	279.5	10.3	550	2 B98350	hypothetical prote
32	276.5	10.2	575	2 D96585	hypothetical prote
33	273	10.0	684	2 T16072	hypothetical prote
34	271	10.0	528	2 T34941	probable Na+/H+ an
35	271	10.0	581	2 G83189	probable sodium/hy
36	256	9.4	565	2 H82610	sodium/proton exch
37	254	9.3	517	2 AC2070	Na+/H+ antiporter
38	244	9.0	458	2 H75278	probable Na+/H+ an
39	240	8.8	549	2 AG0441	probable probable
40	239	8.8	682	2 AC1532	probable Na+/H+ an
41	238.5	8.8	563	2 AD1019	probable sodium/hy
42	237	8.7	682	2 AC1175	probable Na+/H+ an
43	236.5	8.7	542	2 C07032	probable integral
44	231	8.5	549	1 H65214	probable Na+/H+ ex
45	230	8.4	549	2 G91259	hypothetical prote

Query Match 62.4%; Score 1698.5; DB 2; Length 457;
Best Local Similarity 74.0%; Pred. No. 9.3e-118;
Matches 333; Conservative 45; Mismatches 51; Indels 21; Gaps 3;

Qy	3	MEVAAALGALYTTSDYASVSYINLFVALLCACIVLGHLLLEENRWVNESITALLIGLCTG	62
Db	2	LDLSLVSKLPSTL-STSDHASVVALNLFVALLCACIVLGHLLLEENRWVNESITALLIGLCTG	60
Qy	63	VVLLMTKGSKSHLFVSEDLFFIYLLPPIIFNAGFQVKKOFFRNFMTITLFGAVGTMI	122
Db	61	VILLISKGSKSHLLVFSEDLFFIYLLPPIIFNAGFQVKKOFFRNFVTIMLFGAVGTII	120
Qy	123	SFFTISIAAIAIFSRMNTGTLDVGDLAIGAFATDSVCTQLVNLQDETFFLSLVFGE	182
Db	121	SCITISLGTQFFKKLDIGTDLGDLAIGAFATDSVCTQLVNLQDETFFLSLVFGE	180
Qy	183	GVNDATTSIVLFNALQNFDLVHDAVVLKFLGNFFYLFSLSTFLGV-----F	230
Db	181	GVNDATTSVVFNALQSFDLTHLNEAFAHLLGNFLYLFLLSTLLGAASVFLSFLPFL	240
Qy	231	AGLLSAYIKKLYIG-----RHSTDRVALMMLMAYLSYMLAELDLDSGLITVPCG	282
Db	241	TGLISAYVIKKLYFCRWPHINCHRHSTDRVALMMLMAYLSYMLAELFDLSGLITVPCG	300
Qy	283	IWMSHYTHWNTSESSRVTTKHAFTLSFAETFFLYVGMALDLEKWEFASDRPGSIG	342
Db	301	IWMSHYTHWNTSESSRVTTKHTFATLSFAETFFLYVGMALDIDKWRSSVSDTPGTGIA	360
Qy	343	ISSILLGLVIGRAAFVFLPSLSNLTKKAPNEKITWQQVYVWAGLMRGAVSTALAYN	402
Db	361	VSSILLMGLVWVGRAAFVFLPSLSNLAKKNQSEKINFNQVYVWWSGLMRGAVSMALAYN	420

QY 403 KFTBSGHTQLHGNAIMTSTITVVFSTMV 432
Db 421 KFTBSGHTVRGNAIMTSTITVVFSTMV 450

RESULT 2

T22848
hypothetical protein F57C7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22848
R:White, S.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19625

A:Accession: T22848

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-629 <WIL>

A:Cross-references: EMBL:Z69646; PIDN:CAA93476.1; GSPDB:GN00028; CESP:F57C7.2

A:Experimental source: clone F57C7

C:Genetics:

A:Gene: CESP:F57C7.2

A:Map position: X

A:Introns: 33/3; 81/1; 119/2; 155/3; 207/2; 239/1; 274/2; 304/1; 354/1; 386/3; 421/3; 457/2

Query Match 20.8%; Score 567.5; DB 2; Length 629;

Best Local Similarity 29.7%; Pred. No. 3.6e-34;

Matches 160; Conservative 94; Mismatches 182; Indels 103; Gaps 16;

QY 3 MEVAAARLALYTTSDYASVSVINFLVACIVLGHLEEN--RWNESITALLIGLC 60

Db 27 LDMAAQRASNIHRMD---TIIILTIVSVVILVITAWAFKHYRFRFHESGVTLYGLL 83

QY 61 TGVVIL-----LMTGKS----- 73

Db 84 IGVIRYFGLQLQSTQFVITKNTIVKEPPDYLMLVKEGGSVSPHYELIEGFAD 143

QY 74 -----SHLFVSEDLFFIYLLPPIIFNAGFOVKKKOFFRNFMTITLFGAVGTMIISF 124

Db 144 KRKKIEQOEKQSVFSEVFNKLPPIIFNAGYSLKKRHFNRNIGSILAIYFVIGTITSC 203

QY 125 FVISAATAIFSRMNIIGTLVDGDFLAIGAIFSATDSVCTLOVLN-QDETPFLYSLVFGG 183

Db 204 FTGCLMFVFTIFQMG-YSPKELLFFGALISATDPVTIISVENDMNVEADLFAIFGGS 262

QY 184 VYNDATSVLFLNALQNLVDHDAVVKFLGN---FFYFLSSTFLGVFAGLLSAYTI 239

Db 263 ALNDAAVILSEVIEFST--SSEAITLQDFGSAIAGFAGVFFGSLMLGFMIGCMNAFLT 320

QY 240 KKLXIGRHSSTDREVALMMLMAYSLMFLDLGLTGVFCGIVMNSHYTHNVTESSRV 299

Db 321 KMTLISEHAL-LESSLFLVISYFLVAFCVCLTGIVSVLFCGIAQAHYTYNNLSDESQS 379

QY 300 TKHAFATLSFAETFLYVGMAL--DIEKWEFASDRPKGSGISGILLGLVLT--GR 355

Db 380 NTKHFFHMYSEIMESFICIVGSVFVNNQWSP-----SFLLESLSITASR 428

QY 356 AAFVPLFLSLNLTAKAPNEKTWQVQVIVWAGLMRGAVSIALAYNFTSGHTQLHGN 415

Db 429 ALFYVPLSWLLNIRRR--PKIPRYOHMILFAGL-RGAMAFALA-----GRNTSTENR 478

QY 416 AIMTSTITVVFSTMVFGMMTKPLIRLLPASGHPVTSE-----PSSPKSLHSPL 466

Db 479 QMIFATTAVVIVTVLVNGGLTSMWIDYLOIKHKGDAIEEGQRLNENSSSPADQHSOL 537

RESULT 3

T26529

hypothetical protein Y18D10A.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26529

R:Harris, B.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z20226

A:Accession: T26529

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-703 <WIL>

A:Cross-references: EMBL:AL034393; PIDN:CAA22320.1; CESP:Y18D10A.6

A:Experimental source: clone Y18D10A

C:Genetics:

A:Gene: CESP:Y18D10A.6

A:Introns: 23/3; 56/1; 103/2; 246/3; 352/3; 492/2; 578/3

Query Match 20.7%; Score 564.5; DB 2; Length 703;

Best Local Similarity 34.2%; Pred. No. 6.8e-34;

Matches 156; Conservative 83; Mismatches 168; Indels 49; Gaps 16;

QY 7 AARLALYTTSDYASVSVINFLVACIVLGHLEENRWNESITALLIGLCTGVVIL 66

Db 118 AAVGNVSEKKKSLAIFLIVMLATLVVHMLIVSKIHMPESLAIVALGALIG-SIL 176

QY 67 LMTGKSSHLVFESEDLFFIYLLPPIIFNAGFOVKKKOFFRNFMTITLFGAVGTMIISF 126

Db 177 SYRRDSEIEALSPDVFFLVLLPPIIFENAYNLKGYFSEFVPIITFAIFGTISAMV 236

QY 127 ISIAAIAIFSRMNIIGTLVDGDF-----LAIGAIFSATDSVCTLOVLNDET-PFLYSLV 180

Db 237 IG-AGLYILGALG-----IFETFFECFAFAMISAVDPVGTIAIQAVVESLLYMLVF 291

QY 181 GEGVNDATSVL-----FNALQNLVDHDAVVKFLGNFFYFLSSTFLGV 229

Db 292 GESMLNDASVILVATLRAHAKPSFNSLPAEI--ITSAPV-----TFTMEFFESACLV 344

QY 230 FAGLSAYIICKLYIGRHSSTDREVALMMLMAYSLMFLDLGLTGVFCGIVMNSHYT 289

Db 345 GICLLSALLFKHVDL-RKTPSELEFALLIFSIYFGAALDUSGMAILFCGISMST 403

QY 290 WINVTESSRVTKHAFATLSFAETFLYVGMALDIEKWEFASDRPKGSGISGILLG 349

Db 404 RHNVSIAQITFRHTPTISFAETSTFAVIGMAFTI-KLNEFA-----PWLIFWSVV-- 455

QY 350 LVLCRAAFVPLFLSLNLTAKAPNEKTWQVQVIVWAGLMRGAVSIALA-YNKFTSRG 408

Db 456 LCLGRACNVFLVAVLVNOCRK--DVOISMKNOIMFSG-MRGAYCFALVLYMDLKD-- 510

QY 409 HPQLHGNAIMTSTITVVFSTMVFGMMTKPLIRLL 444

Db 511 ----EKKSSILLTVLILFTTIFLGGSSALPFI 542

RESULT 4

T37706

probable sodium/hydrogen exchanger - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: T37706

R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1997

A:Reference number: Z21738

A:Accession: T37706

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-569 <MUR>

A:Cross-references: EMBL:Z97208; PIDN:CAB10103.1; GSPDB:GN000066; SPDB:SPAC15A10.06

A:Experimental source: strain 972h; cosmid c15A10

C:Genetics:

A:Gene: SPDB:SPAC15A10.06

A:Map position: 1

A:Introns: 11/1; 116/3; 356/3

C:Superfamily: hypothetical protein ywg9

Query Match

Best Local Similarity

20.3%; Score 552; DB 2; Length 569;

29.4%; Pred. No. 4.4e-33;

Matches 148; Conservative 113; Mismatches 195; Indels 48; Gaps 15;

QY 27 LFVALLCACIVLGHLL-----ENRWVNESITALLIGCTGVVILLMTKGSLSHLVVF 79
 Db 37 LFILV--LLIGALLTSYVQSKIRAIHETVTSVFGVMVGLIIRVSPGLIIQNMVSF 93
 QY 80 SEDLEFVLLPLPIFNAGFOVKKOFFERNMTITLFGAVGTMSFFTTISAAIAIFSRMN 139
 Db 94 HSTYFNVLLPPIILNSGTLGHOSFRNIGTILTFAGAGTISAVTLCV-LVIFSPLN 152
 QY 140 IGLTVG--DFLAIGAIFSDSVCTQLVQNO---DETPFLYSIVFGGVNDATSIYLF 194
 Db 153 PENLSMTFVEALSMGATLSATDPVTVLAIFNSYKVDQK-LVTIIFGESILNDVAIVMF 210
 QY 195 NALQNFDLVHIDAANVLKFNFFLFLSSFLGVFAGLLSAYIIKKIYIIGHSTDRVA 254
 Db 211 ETLOOFQOGKTLFFLFSIGIGITFTTIFSLIGISGLITALLKYSYLRYS-IFSC 269
 QY 255 LMLMAYLSYMLAEILLDLSGILTVFCGIVMWSHYTHNVTESSRVTTKHAFAFIET 314
 Db 270 IILLMAYTSYFNSCHMSGVVSLFLCGITLKHAFYFNSYKAKLTKYFVRLAQLSEN 329
 QY 315 FLFLYVGMDALDIKWEFASDRPGKSGISILLGLVLIGRAAF--VPFLSFLSLTKKA 372
 Db 330 FIFIVLMSLET-----QVDLVYKPI--FILITVAVTASRYMNVPLSLNLLKPHRQ 380
 QY 373 PN-----EKTWRQOVVIMWAGLMRGAVSIALAYNKFTSGTOLHGNAMITSTIVLVF 428
 Db 381 RGNGLIDHIPYSYQMLFVAGL-RGAVGVLAAGFEGENAQT-----LRATTILVVVVL 432
 QY 429 STMVGMGNTKPLIRLLPASGHPVTSPPSKSLHSPLLTSMQSDLESTTNIVRPSLR 488
 Db 433 TLIIFGTTARMLLEIHIETG--VAADVSDTEIGMLPQQSPFEDLNSAMELSDASAE 490
 QY 489 MLLTKPTHTVHYWRKFDALMRP 512
 Db 491 PVVVDQQTTEH----FDEGNIAF 510

RESULT 5
 S69734
 Hypothetical protein YDR456w - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
 C:Accession: S69734
 R:Dietrich, F.S.
 submitted to the EMBL Data Library, August 1995
 A:Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and 9411
 A:Reference number: S69555
 A:Accession: S69734
 A:Molecule type: DNA
 A:Residues: 1-633 <DIE>
 A:Cross-references: EMBL:U33007; NID:g927685; PID:g927695; GSPDB:GN000004; MIPS:YDR456w
 C:Genetics:
 A:Gene: SGD:NHX1; MIPS:YDR456w
 A:Cross-references: SGD:S0002864
 A:Map position: 4R
 C:Superfamily: hypothetical protein yv9p

Query Match 19.6%; Score 533; DB 2; Length 633;
 Best Local Similarity 26.2%; Pred. No. 1.3e-31;
 Matches 153; Conservative 127; Mismatches 190; Indels 114; Gaps 20;

QY 16 TSDYASVSNLFAVLLCACIVLGHLEEN--RWVNESITALLIGCTGVVILLMTKGS 73
 Db 55 TEEMFSSWALLFILLLSALWSSYYLTQKRIRAVHTVLSIFYGIVGLIIRMSPGHYI 114
 QY 74 SHLFVSEDLFFIYLLPPIIFNAGFOVKKKQFFERNMTITLFGAVGTMSFFTTISAAIA 133
 Db 115 QDVTNNSYFPNVLLPPIILNSGYELNQVNFNNMLSLIIPAOTFTISAVVIGI-ILY 173
 QY 134 IFSRMNIGTLV--GDFLAIGATFSATDSVCTQLVQNODET-PFLYSIVFGGVNDATSIY 190
 Db 134 IFSRMNIGTLV--GDFLAIGATFSATDSVCTQLVQNODET-PFLYSIVFGGVNDATSIY 190

Db 174 IWTFLGLESIDISFADAMSVGATLSATDPVTILSIFNAYKVDPKLYTIIFGESLLNDAIS 233
 QY 191 IVLPNALQNFDLVHIDAANVLKFNFFLFLSTFLGVFAGLLSAYIIKKIYIGHST 250
 Db 234 IVMFETCQKFGQPATFSVVFEGAGLFLMTFSVLLGLVGLILVALLKHTHIRRY-PQ 292
 QY 251 REVALMMLMAYLSYMLAEILLDLSGILTVFCGIVMWSHYTHNVTESSRVTTKHAFAFLSF 310
 Db 293 IESCLILLIAYESYFNSCHMSGIVSLFLCGITLKHAYYNNMSRQJTIKIFYOLLAR 352
 QY 311 IAEFTFLYVGMDAL-DIEKWEFASDRPGKSGISILLGL----VLIGRAAFVPLPS-- 363
 Db 353 LSENFIYILGLELTFEVE-----LVYKPLLIIVAAISICVARCAVFLPSQF 400
 QY 364 -----FLSNLTKK---APNEKITWRQOVVIMWAGLMRGAVSIALAYN-----KF 404
 Db 401 VNWYRVKTTIRMSGITGENISVPDE-IPVNYQMTFWAGL-RGAVGVLAALGIQGYKF 458
 QY 405 TRSGHTQLHGNAMITSTIVVLFSTVFMVGMNTKPLIRLLPASGHPVTSPPSK--SL 462
 Db 459 T-----LLATVILVVVLTIVIFGTTAGMLEVLNKTG-CISEEDTSDDEEDI 505
 QY 463 HSP-LLTSMQSDLE-----STT----- 479
 Db 506 EAPRAINLLNGSSITQDTLGPYSDNNSPDISDQFAVSSNKNLPNNISTTGTGTEGLNET 565
 QY 480 -----NIVRPS-----SLRMLLTKPTHTVHYWRKFDALMRP 514
 Db 566 ENTSPNPARSMDRNRNLRDKLGTIFNSDSQMFQNFQVLPKPVF 609

RESULT 6
 A40205
 Na+/H+-exchanging protein 3 - rabbit
 N:Alternate names: Na+/H+ antiporter
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
 C:Accession: A40205
 R:Tse, C.M.; Brant, S.R.; Walker, M.S.; Pouyssegur, J.; Donowitz, M.
 J. Biol. Chem. 267, 9340-9346, 1992
 A:Title: Cloning and sequencing of a rabbit cDNA encoding an intestinal and kidney sp
 A:Reference number: A40205; MUID:92250540; PMID:1374392
 A:Accession: A40205
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-832 <TSE>
 A:Cross-references: GB:M87007; NID:g165548; PIDN:AAA31420.1; PID:g165549
 C:Keywords: transmembrane protein

Query Match 18.1%; Score 492; DB 2; Length 832;
 Best Local Similarity 31.3%; Pred. No. 1.8e-28;
 Matches 143; Conservative 91; Mismatches 171; Indels 52; Gaps 18;

QY 25 INLFVALLCACIVLGHLEEN--RWVNESITALLIGCTGVVILLMTKGSLSL--FVPESE 81
 Db 57 TALVVLVASLAKIVFHLSHKVTSSVVPESALLVGLVGLGIVL-----AADHIAFTTTP 111
 QY 82 DLFFIYLLPPIIFNAGFOVKKKQFFERNMTITLFGAVGTMSFFTTISAAIAIFSRMIG 141
 Db 112 TVFFIYLLPPIIVLDAGYFMPNRLFFSNLGSILLIYAVGTVWNAATGLSLGVFLSGIMG 171
 QY 142 TLIDVG--DFLAIGATFSATDSVCTQLVQNO-DETPFLYSIVFGGVNDATSIYVFNALQ 198
 Db 172 ELKIGLDFLLGSLIAAADVPAVLAVFEVHVNEVLFIVFEGESULLNDVAVTVVLYNFQ 231
 QY 199 NFDLVHIDAAN--VLKFLGNFFFLSTFLG-VFAGLLSAYIIKKIYIIGHSTDRVA 254
 Db 232 SEVTLGGDKVTGDCVKGIVSEFVYSLGTLGVVFAFLLS--LVTR--FTKHVRVIEPG 287
 QY 255 LMLMAYLSYMLAEILLDLSGILTVFCGIVMWSHYTHNVTESSRVTTKHAFAFIET 314
 Db 288 FVFIISYLSYLTSEMILSLSSILLAITFCGICCKYKANKANISEQSAATVRYTKMKLASGAET 347

```

315 FFLYVGMADLDTKEKFEFSDRPGKSGIGSSILLGLVLIG--RAAFVFFLSFLSNLTAK 372
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
348 IIFMFLGISAVDPLIWTW-----NTAFVLLTLLFYSVERAIGVLIQTWLLNRYRMV 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
373 PNEKITWRQOVVITWAGLMRGVSIAlAYNKKTRSGHTOLHGNAI---MITSTITVILF 428
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
399 QLELI---DOVVMYSYGL-RGAVAFALV-----ALLDGNKVKKEKLNLFVSTTIIWVF 445
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
429 STWVF-GMMTKPLIR-LLLPSAGHPVTSEPPSPKSLH 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
446 FTWIFQGLTIKPLVQWLKVKRSEH---REPKLNKELH 479
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
A46747
Na+/H+-exchanging protein NHE-2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1999
C:Accession: A46747
R:Tse, C.M.; Levine, S.A.; Yun, C.H.; Montrose, M.H.; Little, P.J.; Pouyssegur, J. Biol. Chem. 268, 11917-11924, 1993
A:Title: Cloning and expression of a rabbit cDNA encoding a serum-activated
A:Reference number: A46747; MUID:94280159; PMID:7685025
A:Accession: A46747
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-809 <TSE>
A:Experimental source: ileal villus cells
A:Note: sequence extracted from NCBI backbone (NCBIN:133350, NCBIPI:133351)

```

Na⁺/H⁺-exchanging protein - rabbit

N:Alternate names: Na⁺/H⁺ antiporter; Na⁺/H⁺ exchanger; pH regulatory protein

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-2000

C:Accession: S16328; S13926; S30602

R:Seq. C.M.; Ma, A.I.; Yang, V.W.; Watson, A.J.M.; Levine, S.; Montrose, M.H.; Potter EMBO J. 10, 1957-1967, 1991

A:Title: Molecular cloning and expression of a cDNA encoding the rabbit ileal villus Na⁺/H⁺ exchanger

A:Reference number: S16328; MUID:91293066; PMID:1712287

A:Accession: S16328

A:Molecule type: mRNA

A:Residues: 1-816 <TSE>

A:Cross-references: EMBL:X59935; NID:g1642; PIDN:CAA42558.1; PID:g1643

R:Fliegel, L.; Sardet, C.; Pouyssegur, J.; Barr, A. FEBS Lett. 279, 25-29, 1991

A:Title: Identification of the protein and cDNA of the cardiac Na⁺/H⁺ exchanger.

A:Reference number: S13926; MUID:91138752; PMID:1704856

A:Accession: S13926

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 472-816 <FLI>

A:Cross-references: EMBL:X56536; NID:g1666; PIDN:CAA39881.1; PID:g1667

R:Hildebrandt, F.; Pizzonia, J.H.; Reilly, R.F.; Reboucas, N.A.; Sardet, C.; Pouyssegur Biochim. Biophys. Acta 1129, 105-108, 1991

A:Title: Cloning, sequence, and tissue distribution of a rabbit renal Na⁺/H⁺ exchanger

A:Reference number: S30602; MUID:92096447; PMID:1661611

A:Accession: S30602

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-241, 'A', 243-568, 'E', 570-816 <HIL>

A:Cross-references: EMBL:X61504; NID:g1653; PIDN:CAA43721.1; PID:g1654

A:Note: the authors translated the codon CTG for residue 646 as Val and GCG for residue 647 as Gly

C:Keywords: glycoprotein; transmembrane protein

F:16-35/Domain: transmembrane #status predicted <TM1>

F:108-127/Domain: transmembrane #status predicted <TM2>

F:130-149/Domain: transmembrane #status predicted <TM3>

F:155-174/Domain: transmembrane #status predicted <TM4>

F:192-211/Domain: transmembrane #status predicted <TM5>

F:295-315/Domain: transmembrane #status predicted <TM6>

F:339-357/Domain: transmembrane #status predicted <TM7>

F:387-406/Domain: transmembrane #status predicted <TM8>

F:411-430/Domain: transmembrane #status predicted <TM9>

F:481-500/Domain: transmembrane #status predicted <TM10>

F:757-370/Binding site: carbohydrate (Asn) (covalent) #status predicted

Qy 365 LSNLTAKAPNEKITWROQVVIWAGLMRGAVSIALAYNKKETRSCHTOLHGNAMITSTIT 424
 Db 435 FIN---KPRIVKLPKQDFIAYGGL-RGAIAFSLGV--LLDKKHFFPMCD--LFLTAIT 486
 Qy 425 VVLFSTWVFGMTKPLRLILPASGHPVTSEPPSPKSLHSPPLTSMOGLDLESTTNIVRP 484
 Db 487 VIFTFVVOGNTIRPLVDLL-----AVKKOETKRSINEEIHQTQDLHLTLTGIEDIC-- 538
 Qy 485 SSLRMLLTAKPHVTWHYVYWRKFDLALMR 511
 Db 539 -----GHYGHHWK---DKLNR 552

RESULT 9
 B40204
 Na+/H+-exchanging protein 3 - rat
 N:Alternate names: Na+/H+ antiporter
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
 C:Accession: B40204
 R:Orlowski, J.; Kandasamy, R.A.; Shull, G.E.
 J. Biol. Chem. 267, 9331-9339, 1992
 A:Title: Molecular cloning of putative members of the Na/H exchanger gene family. cDNA
 rally related proteins.
 A:Reference number: A40204; MUID:92250539; PMID:1577762
 A:Accession: B40204
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-831 <ORL>
 A:Cross-references: GB:M85300; NID:g205706; PIDN:AAA41702.1; PID:g205707
 C:Keywords: transmembrane protein

Query Match 17.7%; Score 480.5; DB 2; Length 831;
 Best Local Similarity 28.6%; Pred. No. 1.3e-27;
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;

Qy 22 VVSNLFAVALLCACIV-LGHLEENRWVNESITALLIGLCGVVILLMTKCKSHL--FV 78
 Db 54 IIALMILVASLAKIVFHLSH--KVTSVVPESALLIVIGLVGGIV-----WAADHIAST 106
 Qy 79 FSEDLFYLLPPIIFNAGQVKKQFFRNFTITLFGAVGTMLSPFTTISIAAIAFSRM 138
 Db 107 LPTLTFEYLLPPIVLDAGYEMPNRLFPGLTILLYAVIGTINNAATGLSLYGVFLSG 166
 Qy 139 NGITLDVG--DFLAIGAIFSDTCTQLVNO--DETFFLSLVFEGGVNDATSIVLFN 195
 Db 167 LMGEUKIGLLDPLFGSLIAAVDPVAVLAVFEVHVNEVFLIIFVFGESLLNDATVIVLYN 226
 Qy 196 ALQNFEDLVHIDAIV--VLKELGNFFYLLFSLSTFLGV--FAGLLSAYIIKKLYIGRHSTDR 251
 Db 227 VPESFVTLGGDAVTCVCKGIVSFVYSLGTLGVVIFAFLLS--LVTR--FTKHVRII 282
 Qy 252 EVALMMLMAYLSYMLAEILLDLSGILTVEFCGIVMNSHYTHWNVTSRRVTTKHATLSFI 311
 Db 283 EPGFVFVSYLSYLTSEMLSLAISAILAITFCGICQKQYVYKANISEQATTVRYTKMLASG 342
 Qy 312 ATEFLVYGMADALDIEKWEASDRPGKSGISGTSLLGLVLIG--RAAFVPLPFLSLNLT 369
 Db 343 AETIIFMFLIGISAVDPVITW-----NTAFVLLLVFLSVYRAIGVVLQWILNRY 393
 Qy 370 KKAPNEKITWROQVVIWAGLMRGAVSIALAYNKKETRSCHTOLHGNAMITSTITVILFS 429
 Db 394 RMVQLETI--DQVMSYGGGL-RGAVAYALV-----VLLDEKKVKEKFLVSTLIVVFT 445
 Qy 430 TWVFGMTKPLRLILPASGHPVTSEPPSPKSLH-----SPLTSMOGLDLESTTNIVRPS 485
 Db 446 VIFQGLTIKPLVQWLKVRSE--QREPKLNEKLHGRAFDHILSATIEDISGQIGHNLYRDK 503
 Qy 486 SLRMLLTAKPHVTWHYVYWRKFD-----DALMR 511
 Db 504 -----WSNFDKRLSKVLMLR 518

RESULT 10
 A46748
 Na+/H+-exchanging protein NHE-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A46748; A47449
 R:Wang, Z.; Orlowski, J.; Shull, G.E.
 J. Biol. Chem. 268, 11925-11928, 1993
 A:Title: Primary structure and functional expression of a novel gastrointestinal isof
 A:Reference number: A46748; MUID:93280160; PMID:7685026
 A:Accession: A46748
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-813 <WAN>
 A:Cross-references: GB:L11236; NID:g205318; PIDN:AAA72350.1; PID:g205319
 R:Collins, J.F.; Honda, T.; Knobel, S.; Bulus, N.M.; Conary, J.; DuBois, R.; Ghishan,
 Proc. Natl. Acad. Sci. U.S.A. 90, 3938-3942, 1993
 A:Title: Molecular cloning, sequencing, tissue distribution, and functional expressio
 A:Reference number: A47449; MUID:93248205; PMID:7683411
 A:Accession: A47449
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 117-813 <COL>
 A:Experimental source: intestine
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:130778, NCBI:P:130779)

Query Match 17.6%; Score 479; DB 2; Length 813;
 Best Local Similarity 27.3%; Pred. No. 1.6e-27;
 Matches 143; Conservative 95; Mismatches 206; Indels 80; Gaps 19;

Qy 16 TSDYASV---VSINLFAVALLCACIVLGHLEE-NRWVNESITALLIGLCGVVILLMTKG 71
 Db 73 TLDYPHVQIPFETLWILLASLAKIGFHLXKLPVTPESCILLIMVGLLGGIFGVDE- 131
 Qy 72 KSHLFFSEDLFFIYLLPPIIFNAGQVKKQFFRNFTITLFGAVGTMLSPFTTISIAA 131
 Db 132 KSPD--AMKTDVFFLYLLPPIVLDAGYEMPTRPFFENLGTIFWYAVVGTLLNSIGIGLSL 189
 Qy 132 IATFSRNIGTLDVG--DFLAIGAIFSDTCTQLV--NODETFFLSLVFEGGVVND 188
 Db 190 FGICQIEAFGLSDITLLQNLFLGSLISAVDPVAVLAVFENIHVNEQLIYLVFGESLLND 249
 Qy 189 TSIVLFNALQNF-DLVHIDAIVLKFELGNFFYLLFSLSTFLGVFAGLSAY-----I 238
 Db 250 VTVVLYNLFKSFQCMKTIQTVDFAGIANFVVGIGGVIGLIGLFGIAAFTTRFTHIRV 309
 Qy 239 IKKLYIGRHSTDRVALMMLMAYLSYMLAEILLDLSGILTVEFCGIVMNSHYTHWNVTESSR 298
 Db 310 IEPFLV-----FLYSLSYITAEFHLSGIMAITACAMTNKYVEENVOSKSY 357
 Qy 299 VTTKHAFATLSIAETFLYVVGMDAL-DIEKWEFASDRPGKSGISGTSLLGLVLIGRAA 357
 Db 358 TTIKYFMKMLSSVSETLIFPMGVSTVYKHNHWA-----FVCFTLAFLIWRAL 408
 Qy 358 FVPLFSLNLTAKAPNEKITWROQVVIWAGLMRGAVSIALAY-----NKFTSGHTQLH 413
 Db 409 GVEVLTVQVNWFRTP--LTFKQDFIAYGGL-RGAICFALVFLPATVPR----- 457
 Qy 414 GNAMITSTITVILFSTWFGVGMKPLIRLLPASGHPVTSEPPSPKSLHSPPLTSMOQS 473
 Db 458 -KKLFIATAIVVIEFTVILGITIRPLVFEVLDVKKRSN--KKQAVSBEIHCRFDHVK-T 513
 Qy 474 DLESTTNIVRPSLRLTTPHTVHYVYWR-----KFDALMRPM 513
 Db 514 GIEDVCG-----HWGNFWRDKFKKDDKYLRLK 542

RESULT 11
 S30198
 Na+/H+-exchanging protein - Chinese hamster
 N:Alternate names: Na+/H+ antiporter; Na+/H+ exchanger
 C:Species: Cricetus griseus (Chinese hamster)

[illegible]

A:Residues: 1-814, 'SNARSRQRLSHRLFHQSRGCGWGLPLPLTRIGPAPPPTAWOLGPOPPQHSSSPAASREASSPELH
C:Genetics:
A:Gene: GDB:SLC9A1; APNH; NHE1
A:Cross-references: GDB:119683; OMIM:107310
A:Map position: lp36.1-lp35
C:Keywords: glycoprotein; transmembrane protein
F:75,370,410/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.48; Score 474; DB 2; Length 815;
Best Local Similarity 28.8%; Pred. No. 3.8e-27;
Matches 146; Conservative 96; Mismatches 203; Indels 62; Gaps 19;

QY 18 DYASV---VSNLFAVLCACVILGHLEE--NRWNESITALIIGLCTGVVILLMTKGKS 73
DB 95 DYTHVPTFEISLWLLACLAKMGHFIPTISSIVPESCLIVVGLLVGLI---KGVG 150
QY 74 SHLFVSEDLFFIYLLPIIFNAGQVKKKOFFRNMFTITLFGAVGTWISFETIS--IAA 131
DB 151 ETPPFLQSDVFFFLPPIILDAGYFLRQFTENLGLTILFAVVGTLWNAFFLGLMYA 210
QY 132 TAIFSRMIGILDVGDFLAIGAIFSATDSVCTLOVLNDE--TPFLYSLVFGGVNDATS 190
DB 211 VCLVGEQINNIGLDNLLFGSIISAVDPVAVLAVFEEIHINELLHLVFGESLNDVAT 270
QY 191 IVFNALQNF--DLVHIDAAYVLFKFLG--NFFYFLSSTFLGVFAGLLSAYIIKKLYIGH 247
DB 271 VLYHLFEEFANYEV--GIVDFLGLFISFFVVALGVGVVGVVIAAFTSR---FTSH 325
QY 248 STDREVALMLMAYLSYLAELLDLSGLTIVFFCGIVMSHYTHWNVTSSRVTTKHAFAT 307
DB 326 IRVIEPLFVLYSYMAYLSAELFHLSGIMALIASGVVMRYPVEANISHKSHHTTKYFLKM 385
QY 308 LSFIAETFLYVGVMDALDIE---KWEFASDRPKSGISILLGLVLIGRAAFVPLSFL 364
DB 386 WSSVSETLIFLVGVSTVAGSHHWNTEV-----ISTLL--FCLIAVGLVGLUTW 434
QY 365 LSNLTKKAPNEKITRQOVVIMWAGLMRGAVSIALAYNKFTSRGHTQLHGNAMITSTIT 424
DB 435 FIN---KPRIVLTKPKDQFIYAGGL--RGAIATFSLGY--LLDKKHFPWCD--LFLTAIT 486
QY 425 VVLFSTVFGMMTKPLIRLLLPASGHPVTSEPSKSLHSPFVSEDLFFIYLLPIIFNAGQVKKKOFFR 484
DB 487 VIFFTVFVGGMTIRPLVDLL-----AVKKQKTRKRSINEEHTQFLDHLTLTGIEDIC-- 538
QY 485 SSRLMLTKPTHTVHYWKRKFDALMR 511
DB 539 -----GHYGHWNK---DKLNR 552

RESULT 14
A46188
CAMP-activated Na+/H+-exchanging protein betanHE - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C:Accession: A46188
R:Borgese, F.; Sartet, C.; Cappadoro, M.; Pouyssegur, J.; Motaïs, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 6765-6769, 1992
A:Title: Cloning and expression of a cAMP-activated Na+/H+ exchanger: evidence that the
A:Reference number: A46188; MUID:92357712; PMID:1379718
A:Accession: A46188
A:Status: preliminary
A:Molecule type: nucleic acid
A:Experimental source: cephalic kidney hematopoietic tissues
A>Note: sequence extracted from NCBI backbone (NCBI:113525)

Query Match 17.3%; Score 472; DB 2; Length 759;
Best Local Similarity 28.7%; Pred. No. 4.9e-27;
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;

QY 31 LLCACIVLG--HLEE--NRWNESITALIIGLCTGVVILLMTKGKSHLFFVSEDLFFIYL 88
DB 78 LLALLMKLGFHLIPRLSAVVPESCLIVVGLLVGLIKVIGEPD---VLDSQLFFLCL 133

QY 89 LPPIFNAGQVKKKOFFRNMFTITLFGAVGTWISFETIS--IAAIFSRMNIPTLDVG 146
DB 134 LPPIILDAGYFLRPTETENNGTILFPAVIGTLWNAFFMGGLLYALCOIESVGLSGVDLL 193
QY 147 DFLAIGAIFSATDSVCTLOVLNDE--TPFLYSLVFGGVNDATSIVFNALQNFDLVHI 205
DB 194 ACLFGSIVSAVDPVAVLAVFEEIHINELHILVFGESLNDVAVVLYNLFEEFSKVG- 252
QY 206 DAAVVLKFLG--NFFYFLSSTFLGVFAGLLSAYIIKKLYIGHSTDRVALMMLMAYLS 263
DB 253 TTVLDVFLGVGCVFVSVLGGVLAIGYFLAAFTSR---FTSHTRVIEPLFFFLFYSMA 309
QY 264 YMLAELDLGLSGLTIVFFCGIVMSHYTHWNVTSSRVTTKHAFATLGFIAETFLVXGMD 323
DB 310 YLSEMFHLSGIMALACGVVMRYPVEANISHKSYTTIKYFLKMWSSVSTLIFELGVS 369
QY 324 AL---DIEKWEFASDRPKSGISILLGLVLIGRAAFVPLSFLSNLTKKAPNEKITWR 380
DB 370 TVAGPHANNTEV-----ITTVI--LCLVSRVLGVIGLTFIIN---KFRIVKLTKK 415
QY 381 QOVVIMWAGLMRGAVSIALAYNKFTSRGHTQLHGNAMITSTITVVLFTSWFVGMKTKPL 440
DB 416 DQFTVAYGGL--RGAIATFSLGY--LLSNHQMNRN--LFLTAITVITVFFTVFVGGMTIRPL 469
QY 441 IRLLPASGHPVTSEPSKSLHSP---LTSMQGSDLESTTNIVRPSLSRLMLTKPTH 496
DB 470 VELL--AVKKKSKPSINEEHTFEDHLTLTGVEG-----VCGH 507
QY 497 TVHYWKRK 504
DB 508 YGHYWNKE 515

RESULT 15
A40204
Na+/H+-exchanging protein 1 - rat
N:Alternate names: Na+/H+ antiporter
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 28-Feb-1997
C:Accession: A40204
R:Orlowski, J.; Kandasamy, R.A.; Shull, G.E.
J. Biol. Chem. 267, 9331-9339, 1992
A:Title: Molecular cloning of putative
rally related proteins.
A:Reference number: A40204; MUID:92250539; PMID:1577762
A:Accession: A40204
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-820 <ORL>
A:Cross-references: GB:M85299
C:Keywords: transmembrane protein

Query Match 17.0%; Score 463; DB 2; Length 820;
Best Local Similarity 29.3%; Pred. No. 2.5e-26;
Matches 138; Conservative 92; Mismatches 187; Indels 54; Gaps 17;

QY 48 VNESITALIIGLCTGVVILLMTKGKSHLFFVSEDLFFIYLLPIIFNAGQVKKKOFFR 107
DB 133 VPESCLIVVGLLVGLI---KGVGETPPFLQSDVFFFLPPIILDAGYFLRQFTE 188
QY 108 NFMFTITLFGAVGTWISFETIS--IAAIFSRMNIPTLDVGDFLAIGAIFSATDSVCTLO 165
DB 189 NLGHTILFVAVGTUWNAFFLGGILYAVCLVGEQINNIGLDTLLFSIISAVDPVAVLA 248
QY 166 VLNDE--TPFLYSLVFGGVNDATSIVFNALQNF---DLVHIDAAYVLFKLGNFYFLF 221
DB 249 VFEEIHINELLHLVFGESLNDVAVVLYHLFEEFASVYVGI--SDIELGLF--SFEVVS 306
QY 222 LSSTFLGVFAGLLSAYIIKKLYIGHSTDRVALMMLMAYLSYLAELLDLSGLITVFFC 281
DB 307 LGGVFGVGVVGVIAAFTSR---FTSHIRVIEPLFVFLVLYSYMAYLSAELFHLSGIMALIAS 363

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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:42:04 ; Search time 27 Seconds
(without alignments)
821.846 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAAARIGALYTTSQDYA.....GRGFVPFSPGSPTEQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues 112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	19.9	669	1 NAH6_HUMAN	Q92581 homo sapien
2	533	19.6	633	1 NAH2_YEAST	Q04121 saccharomyc
3	492	18.1	832	1 NAH3_RABIT	P26432 oryctolaqus
4	485	17.8	809	1 NAH2_RABIT	P50482 oryctolaqus
5	485	17.8	896	1 NAH5_HUMAN	Q14940 homo sapien
6	482.5	17.7	834	1 NAH3_HUMAN	P48764 homo sapien
7	481	17.7	816	1 NAH1_RABIT	P23791 oryctolaqus
8	480.5	17.7	831	1 NAH3_RAT	P26433 rattus norv
9	480	17.6	812	1 NAH2_HUMAN	Q9ubyo0 homo sapien
10	480	17.6	839	1 NAH3_DIDMA	Q28362 didelphis m
11	479	17.6	813	1 NAH2_RAT	P48763 rattus norv
12	479	17.6	820	1 NAH1_MOUSE	Q61165 mus musculu
13	479	17.6	898	1 NAH5_RAT	Q920x2 rattus norv
14	478	17.6	822	1 NAH1_CRIGR	P48761 cricetulus
15	476	17.5	817	1 NAH1_BOVIN	Q28036 bos taurus
16	476	17.5	818	1 NAH1_PIG	P48762 sus scrofa
17	476	17.5	820	1 NAH1_RAT	P26431 rattus norv
18	474	17.4	815	1 NAH1_HUMAN	P19634 homo sapien
19	472	17.3	759	1 NAH6_ONCMY	Q01345 oncorhynch
20	456	16.8	717	1 NAH4_RAT	P16434 rattus norv
21	395	14.5	651	1 NAH3_CAEEL	O16452 caenorhabdi
22	390	14.3	667	1 NAH9_CAEEL	P35449 caenorhabdi
23	236.5	8.7	542	1 YMB7_MYCTU	Q50678 mycobacteri
24	231	8.5	549	1 YJCE_ECOLI	P32703 escherichia
25	186.5	6.9	578	1 YCGO_ECOLI	P76007 escherichia
26	159	5.8	808	1 NAH2_ZYGRO	Q42701 zygosacchar
27	142.5	5.2	426	1 Y057_METJA	Q60362 methanococc
28	140.5	5.2	791	1 NAH1_ZYGRO	Q99173 zygosacchar
29	139.5	5.1	635	1 SL56_HUMAN	Q9v289 homo sapien
30	138.5	5.1	383	1 NAPA_ENTHR	P26235 enterococcu
31	137.5	5.1	985	1 NAH1_YEAST	Q98271 saccharomyc
32	133.5	4.9	422	1 YF21_METJA	Q58916 methanococc
33	131.5	4.8	759	1 NAH2_SCHPO	O14123 schizosacch

34	129	4.7	636	1 SL56_RABIT	Q9xt77 oryctolaqus
35	128	4.7	504	1 NU5M_ORNAN	Q36459 ornithorhyn
36	125.5	4.6	558	1 YBAL_ECOLI	P39830 escherichia
37	124	4.6	410	1 Y588_BUCAL	P57648 buchnera ap
38	123	4.5	502	1 PUTP_SALTY	P10502 salmoneilla
39	120	4.4	634	1 SL56_RAT	O70247 rattus norv
40	118	4.3	502	1 PUTP_ECOLI	P07117 escherichia
41	117	4.3	430	1 Y0GE_BACSU	P54487 bacillus su
42	116	4.3	492	1 YCLF_BACSU	P94408 bacillus su
43	116	4.3	554	1 NU5M_APILI	P34855 apis mellif
44	115.5	4.2	468	1 NAH_SCHPO	P36606 schizosacch
45	115	4.2	317	1 PSRC_WOLSU	P31077 wolfinella s

ALIGNMENTS

RESULT 1	NAH6_HUMAN	STANDARD;	PRT;	669 AA.
ID	NAH6_HUMAN			
AC	Q92581;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/hydrogen exchanger 6 (Na(+)/H(+) exchanger 6) (NHE-6).			
GN	SLC9A6 OR NHE6 OR KIAA0267.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98175963; PubMed=9507001;			
RA	Numata M., Petrecca K., Lake N., Orłowski J.;			
RT	"Identification of a mitochondrial Na+/H+ exchanger.";			
RL	J. Biol. Chem. 273:6951-6959(1998).			
RN	[2]			
PC	SEQUENCE OF 4-669 FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=97191544; PubMed=9039502;			
RA	Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,			
RT	Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by			
RT	analysis of cDNA clones from cell line KG-1 and brain.";			
RL	DNA Res. 3:321-329(1996).			
CC	-1- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS			
CC	THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME			
CC	AND CALCIUM HOMEOSTASIS.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.			
CC	-1- TISSUE SPECIFICITY: UBIQUITOUS; BUT IS MOST ABUNDANT IN			
CC	MITOCHONDRIUM-RICH TISSUES SUCH AS BRAIN, SKELETAL MUSCLE, AND			
CC	HEART.			
CC	-1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF030409; AAC39643.1; -			
DR	EMBL; D87743; BAA13449.1; -			
DR	Genew; HGNC:11079; SLC9A6.			
DR	MIM; 300231;			
DR	InterPro; IPR000676; Nah_Exchng.			
DR	InterPro; IPR004709; Nah_exchang3.			
DR	Pfam; PF00999; Na_H_Exchange; 1.			
DR	PRINTS; PR01084; NAHEXCHNGR.			
DR	TIGRFAMs; TIGR00840; b.cpal; 1.			
DR	Transmembrane; Transport; Antiport; Sodium transport; Mitochondrion.			
KW				

FT TRANSMEM 28 48 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 142 162 POTENTIAL.
 FT TRANSMEM 179 199 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 FT TRANSMEM 340 360 POTENTIAL.
 FT TRANSMEM 382 402 POTENTIAL.
 FT TRANSMEM 404 424 POTENTIAL.
 FT TRANSMEM 447 467 POTENTIAL.
 FT TRANSMEM 483 503 POTENTIAL.
 SQ SEQUENCE 669 AA; F6416596229F2639 CRC64;

Query Match
 Best Local Similarity 19.9%; Score 541; DB 1; Length 669;
 Matches 104; Conservative 97; Mismatches 210; Indels 78; Gaps 18;

QY 1 MGNEVAARALGALYTTSDYASVSYNLFVALLCACIVLGHLEEN--RWVNESITALIIG 58
 Db 53 MDEIIVSEKQAEHRQDSANLL--IFILLTLTLTWLFKRRARELHETGLAMIYG 109

QY 59 LCTGVV-----ILIMTKKSH--LFFVSEDLFFIYLLPPIIFNAGFOVKK 102
 Db 110 LLVGLVRYGIHVPDNNVNTLSCVQSPTLLVTFDEVENILLPPIIFVAGISLKR 169

QY 103 KOFFRNFMTITLFGAVGTWISFTTISIAAIAFSRNNIGTLDVGF-----LAIGAIFSA 157
 Db 170 RHFRNLGSLIAYAFGLTAISCFVIGSIMYGCVTIMKVTGQLAGDFYFTDCLLFGAIVSA 229

QY 158 TDSVCTLOVNOETPP--LYSLVFGEGVVNDATSI VLENALQNF-----DLVH-IDAENVL 211
 Db 230 TDPVTVLAIFHELOVDVELYALLFGESVLNDAVAIVLSSIVAYQAGDNSHTFDTAMP 289

QY 212 KFLGNFFYFLSTPLGVPAGLLSAYIK--KLYIGRSTDRVALMMLMAYLSYMLAEL 269
 Db 290 KSGIFLGFISGFAMGAATGVVTAIVTKFTKL--REFQQLTGLTFLMSWSTELLAEA 346

QY 270 LDLGILVFFCGIGVMSHYTHNVTESSRVTTKHAFATLSFTAEFTFLYVGMALDEK 329
 Db 347 WGTGVAVAFGCIQAHYTYNNLSTESQHRTKQFELNFIENFIYSMGLTFTFQN 406

QY 330 WEFASDRGKSGISILLGLVLIGRAAFVPLPSLSNLTKAPNEKITWRQVQVWAG 389
 Db 407 HVF---NPTFFVVG---AFVAIFLGRAANIYPLSLLNLGRES---KIGSNFQHMMAFAG 456

QY 390 LMRGAVSIALAYNFTSRGHTQLHGNATMITSTIVVLFSTWVFGMMTKPIRLLLPASG 449
 Db 457 L-RGAMAFALAIR-----DTATYARQMMFSTLLIVFTVWVGGGTAMLSCI----- 504

QY 450 HPVTSESPSKSLHSLPILTSMQGSDLESTTNIVRPSSLRMLLTKPTHVHYVWRKFDAL 509
 Db 505 HIRGVDSQDHLGVP-----ENERTTKASAWLFRM-----WYNFDHNY 545

QY 510 MRPFGRG 518
 Db 546 LKPLTHSG 554

RESULT 2

NAH2_YEAST ID NAH2_YEAST STANDARD; PRT; 633 AA.
 AC Q04121;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitochondrial sodium/hydrogen exchanger (Mitochondrial Na(+)/H(+) exchanger).
 GN NAH2 OR NHX1 OR YDR456W OR D9461.40.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

NCBI_TaxID=4932;
 [1]
 SEQUENCE FROM N.A.
 Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Winant A., Yellon M., Bolstein D., Davis R.W.;
 Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=98175963; PubMed=9507001;
 Numata M., Petrecca K., Lake N., Orlowski J.;
 Identification of a mitochondrial Na+/H+ exchanger.";
 J. Biol. Chem. 273:6951-6959(1998).
 CC -!- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+ ACROSS THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR VOLUME AND CALCIUM HOMEOSTASIS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -----
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 CC -----
 DR EMBL; U33007; AAB64861.1;
 DR SGD; S0002864; NHX1.
 DR InterPro; IPR000676; NaH_Exchange.
 DR InterPro; IPR004709; NaH_Exchange3.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR PRINTS; PR01084; NAHEXCHNGR.
 DR TIGRFAWS; TIGR00840; b_cpai; 1.
 KW Transmembrane; Transport; Antiport; Sodium transport; Mitochondrion.
 FT TRANSMEM 62 82 POTENTIAL.
 FT TRANSMEM 86 106 POTENTIAL.
 FT TRANSMEM 118 138 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 218 238 POTENTIAL.
 FT TRANSMEM 259 279 POTENTIAL.
 FT TRANSMEM 307 327 POTENTIAL.
 FT TRANSMEM 353 373 POTENTIAL.
 FT TRANSMEM 377 397 POTENTIAL.
 FT TRANSMEM 432 452 POTENTIAL.
 FT TRANSMEM 458 478 POTENTIAL.
 SQ SEQUENCE 633 AA; 70147 MW; 9B771ABDE41CEB0A CRC64;

Query Match
 19.6%; Score 533; DB 1; Length 633;
 Best Local Similarity 26.2%; Pred. No. 1.le-27;
 Matches 153; Conservative 127; Mismatches 190; Indels 114; Gaps 20;

QY 16 TSDYASVSYNLFVALLCACIVLGHLEEN--RWVNESITALIIGCTGVVILLMTCKS 73
 Db 55 TEEMFSSWALFIMLLLSIALMSWSSYLTQKRIRAVHETVLSIFGVNGLIRSPGHYI 114

QY 74 SHLEVFSEDLFFIYLLPPIIFNAGFOVKKOFFRNFMTITLFGAVGTWISFTTISIAAIA 133
 Db 115 QDVTFTNSSYFFVLLPPIILNSGYELNQVNFNNMLSILIFAIPTGTFISAVVIGI-ILY 173

QY 134 IFSRNMIGTLDV--GDFLAIGAIFSATDSVCTLOVNOET--PFLYSLVFGEGVVNDAT 190
 Db 174 IWTFLGESIDISFADAMSVGATLSATDPVTLSIFWAYKVDPKLYTIIFGESLNDNIS 233

QY 191 IVLFNALQNFDLVHIDAAYVLLKFLGNFFYFLSTFLGCVFAGLLSAYIIKKLYIGRST 250
 Db 234 IVMFETCQKPHGQPATFSSVFEGAGLFMTFVSLLIGVLIGLVALLLKTHHRRY-PQ 292

QY 251 REVALMMLMAYLSYMLAELDLGILTVFPCGIVMSHYTHNVTESSRVTTKHAFATLSF 310

Db 293 IESCUILLIAYEYFSGCHMSGIVSLFCGILTKHYAYNMSRRSQITIKYFOLLAR 352
Qy 311 IAEITFLYVGMAL-DIEKWEFASDRPGKSGISSILLG----VLIGRAAFVPEPLS-- 363
Db 353 LSENFIFILGLELETEVE-----LVYKPLIITVAALISICVARWCAPVPLSQF 400
Qy 364 -----FLSNLTKK---APNEKITRQOVVIMWAGLMRGAVSIALAYN-----KF 404
Db 401 VNWYIRVKTIKIRSGITENISVPDE-IPYNYQMTTFWAGL-RGAVGVALALGIQGEYKF 458
Qy 405 TRSGHTOLHGNAMITSTITVVLFSTWFGMMTKPLIBELLPASGHPVTSPPSPK--SL 462
Db 459 T-----LLATLVVVVILFVITGGTTAGMLEVLNKTG-CITSEEDTSDDEFDI 505
Qy 463 HSP-LLTSMOGSDLE-----STT----- 479
Db 506 EAPRAINLLNGSIOTDGLPGYSDNNSPDISDOFAVSSNKNLPLNNISTGGTGGGLNET 565
Qy 480 -----NIVRPS-----SLRMLTKPTHVHYWKRKFDALMRPF 514
Db 566 ENTSPNPARSSMDKRNLRDKLGTIFNSDSQWFQNFDEQVLKPVF 609
RESULT 3
ID NAH3_RABIT STANDARD; PRT; 832 AA.
AC P26432.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 3 (NA(+)/H(+) exchanger 3) (NHE-3).
GN SLC9A3 OR NHE3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid:9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE=Ileal villus, and Kidney cortex;
RX MEDLINE=92250540; PubMed=1374392;
RA Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
RT "Cloning and sequencing of a rabbit cDNA encoding an intestinal and
RT kidney-specific Na+/H+ exchanger isoform (NHE-3).";
RL J. Biol. Chem. 267:9340-9346(1992).
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: INTESTINAL AND KIDNEY SPECIFIC. MOST ABUNDANT
CC IN KIDNEY CORTEX, FOLLOWED EQUALLY BY ILEUM AND ASCENDING COLON,
CC THEN KIDNEY MEDULLA AND JEJUNUM. IS ABSENT FROM DUODENUM AND
CC DESCENDING COLON.
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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CC -----
CC EMBL; M87007; AAA31420.1; -.
DR PIR; A40205.
DR InterPro; IPR000676; NaH_Exchange.
DR InterPro; IPR004709; NaH_exchang3.
DR Pfam; PF00999; Na_H_Exchange; 1.

DR PRINTS; PRO1084; NAHEXCHNGR.
DR TIGRams; TIGR00840; D_cpal; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
KW Multigene family; Phosphorylation; Polymorphism.
FT DOMAIN 1 11
FT TRANSMEM 12 27
FT DOMAIN 28 59
FT TRANSMEM 60 79
FT DOMAIN 80 81
FT TRANSMEM 82 101
FT DOMAIN 102 110
FT TRANSMEM 111 130
FT DOMAIN 131 134
FT TRANSMEM 135 154
FT DOMAIN 155 180
FT TRANSMEM 181 200
FT DOMAIN 201 209
FT TRANSMEM 210 229
FT TRANSMEM 230 249
FT TRANSMEM 250 269
FT DOMAIN 270 298
FT TRANSMEM 299 319
FT DOMAIN 320 339
FT TRANSMEM 340 359
FT TRANSMEM 360 366
FT TRANSMEM 367 385
FT DOMAIN 386 435
FT TRANSMEM 436 455
FT DOMAIN 456 832
FT CARBOHYD 325 325
FT VARIANT 144 144
SQ SEQUENCE 832 AA; 92748 MW; 8C8BB7C296CF8740 CRC64; 1
Query Match 18.1%; Score 492; DB 1; Length 832;
Best Local Similarity 31.3%; Pred. No. 6.9e-25;
Matches 143; Conservative 91; Mismatches 171; Indels 52; Gaps 18;
Qy 25 INLFVALLCACIVIGHLLEE-NRWVNESITAIILGLCTGVVILLMTKCKSHL--FVFESE 81
Db 57 IALWVLVASLAKIVFHLSHKVTSSVVPESALLVLGLVGLGVL-----AADHIAFTLTP 111
Qy 82 DLFFIYLLPPIIFNAGFOVKKQFFRNEMTITLFCAGVTMISFFTTISIAAIAIFSRMNG 141
Db 112 TVFFIYLLPPIVDAGYFMPNRLFPFNLGSLIILYAVGTVNNAATGSLXGVFLSGIMG 171
Qy 142 TLDDVG--DFLAIGALFASDTSVCTLOVLNQ--DETDFLYSLVFGVGVDATSVLFLNALQ 198
Db 172 ELKIGLLDFLLFGSLIAAVDPVAVLAVFEVHVNEVLFIVFEGESLLNDVAVTVLYNVFQ 231
Qy 199 NFDLVHIDAAV---VLKELGNFFYFLSSTFLG-VFAGLLSAYIIKKLYIGRHSTDEVA 254
Db 232 SEVTLGGDKVTGDCVKGVISFVYVSLGTLGVVVFALLS--LVTR--FTKHVRVIEPG 287
Qy 255 LMLMAYILSYMLAELLDLISGILTVFFCGIVMSHYTHVNVHTVSSRYTTKHAFATLSFIAET 314
Db 288 FVFIISYLSYLTSEMLSSLIATFCGICCKQYVKANISEQSAATTVRYTKMLASGAET 347
Qy 315 FLFLYVGMALDIEKWEFASDRPGKSGISSILLGLVLIG--RAAFVPLSFLSLNLTKA 372
Db 348 LIIFMFLGISAVDPLIWTW-----NTAFVLLTLFLFVSFVRAIGVQLVTLNRYRMV 398
Qy 373 PNEKITRQOVVIMWAGLMRGAVSIALAYNKTFRSGHTOLHGNAT-----MITSTITVVL 428
Db 399 QLELI---DOVVMYSGGL-RGAVAFALV-----ALLDGNKKNKLFVSTTIIIVVF 445
Qy 429 STMVF-GMMTKPLIR-LLLPASGHPVTSPPSPKSLH 463
Db 446 FTVIFOGTLIKPLVQWLKVRSEH---REPKNLEKLH 479
RESULT 4
ID NAH2_RABIT STANDARD; PRT; 809 AA.

RA Menon A.G.;
 RT "Molecular cloning and physical and genetic mapping of a novel human
 RL Na+/H+ exchanger (NHES/SLC9A5) to chromosome 16q22.1.";
 RL Genomics 25:615-622(1995).
 CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
 CC TRANSDUCTION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, TESTIS, SPLEEN, AND
 CC SKELETAL MUSCLE.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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 CC -----
 CC EMBL: AF111173; AAC98696.1; -.
 CC EMBL: U08607; AAA87678.1; -.
 CC Genew; HGNC:11078; SLC9A5.
 CC MIN; 600477; -.
 CC InterPro; IPR000676; NaH_Exchng.
 CC InterPro; IPR004709; NaH_exchang3.
 CC Pfam; PF00999; Na_H_Exchange; 1.
 CC PRINTS; PR01084; NAHEXCHNGR.
 CC TIGRFAMs; TIGR00840; b_cpai; 1.
 CC Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation.
 FT TRANSMEM 46 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 104 124 POTENTIAL.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 201 221 POTENTIAL.
 FT TRANSMEM 247 267 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT TRANSMEM 332 352 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT TRANSMEM 429 449 POTENTIAL.
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 202 202 L -> V (IN REF. 2).
 FT SEQUENCE 896 AA; B9D234BFE0922269 CRC64;
 Query Match 17.8%; Score 485; DB 1; Length 896;
 Best Local Similarity 29.9%; Pred. No. 2.1e-24;
 Matches 155; Conservative 93; Mismatches 190; Indels 80; Gaps 22;
 QY 22 VVSINLFAVLCACIVLGLHLEE-NRWYNESITALIIGLCTGWIILLMTKGKSSHLFVFS 80
 Db 49 LVALWILVASLAK--IVFSLSRKVTSLVPESCILLGLGLVGLVAVAKAEYQL---E 103
 QY 81 EDLFFIYLLPPIIFNAGFOVKKQFFRNPMTITLFCAGVTMISFFTTISIA-----AIAI 134
 Db 104 PGTFELFLPPIVLDSDGYMPSRLFFDNLGAILTVAVGTLWNAFTTGAALGLQAGLV 163
 QY 135 FSRMNTGTTLDVGDFLAIGAIFATSQVCTQLVNLQ---DETFFLSYLFGEVGVNDVSI 191
 Db 164 APRVQAGLL---DLFLFGLSLISAVDPVAVLAVFEEVHVNET--LFIIIVFGESLLDVAIV 218
 QY 192 VLFNALQNF---DLVHIDAAVVLKGLNFFYFLSLSTFLG-VFAGL--LSAVIITKKLYIG 245
 Db 219 VLYKVCNSFVMSGANVQATDYLVKGVSLFVVSGLGAAGVGLVFAFLALTTRFTRVRI- 277

QY 246 RHSTDREVALMMLMAYLSYMLAEELLDLSGILTVFFCGIVMSHYTHNVNTESSRVTTKHAF 305
 Db 278 -----IEPLLVFLVLAAYLTAEMASISALLAVTMCGLGCKKYVEANISHKSRITVKYTM 332
 QY 306 ATLSFTAETFLFYVGMALDIEKWEFASDRPKSGISISILG----LVLIGRAAFVFL 362
 Db 333 KTLASCAETVIFMLLGISAVDSKAWD-----SGVLGTGLTILFLFRALGVVLQ 382
 QY 363 SFLSNLTKNAPNEKITRQOVVILWAGLMRGAVSIALAYNAKFTRSCHTOLHGNAMITST 422
 Db 383 TWYNQFRVLPLDKI---DOVMSYGL-NGAVAFALV----ILLDTKVPKADYFVAT 434
 QY 423 ITVVFLESTWVFGMMTKPLIR-LLLPASGHPVTSEPSKLSHSLPLTSMQGSDELTNNI 481
 Db 435 IVVVFETVVOGLTIKPLVKWLVKRSEH---HKPTLNQELHEHTDHI-----LAAVEDV 487
 QY 482 VRPSSRLMLLTGKTHVHHY---WRKFD-----DALMR 511
 Db 488 V-----GHHGYHYWRDRWEQFDKKYLSQLLMR 514
 RESULT 6
 NAH3_HUMAN STANDARD; PRT; 834 AA.
 ID NAH3_HUMAN
 AC P48764;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/hydrogen exchanger 3 (Na(+)/H(+)) exchanger 3) (NHE-3).
 GN SUC9A3 OR NHE3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney cortex;
 RX MEDLINE=95358265; PubMed=7631746;
 RA Brant S.R., Yun C.H., Donowitz M., Tse C.-M.;
 RT "Cloning, tissue distribution, and functional analysis of the human
 RT Na+/N+ exchanger isoform, NHE3".
 RL Am. J. Physiol. 269:G198-G206(1995).
 CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
 CC TRANSDUCTION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U28043; AAB48990.1; -.
 CC Genew; HGNC:11073; SLC9A3.
 CC MIN; 182307; -.
 CC InterPro; IPR000676; NaH_Exchng.
 CC InterPro; IPR004709; NaH_exchang3.
 CC Pfam; PF00999; Na_H_Exchange; 1.
 CC PRINTS; PR01084; NAHEXCHNGR.
 CC TIGRFAMs; TIGR00840; b_cpai; 1.
 CC Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 13 24 A (M1) HYDROPHOBIC.

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FT DOMAIN 25 54 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 55 73 B (M2) HYDROPHOBIC.
FT DOMAIN 74 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 C (M3) (POTENTIAL).
FT DOMAIN 100 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 D (M4) (POTENTIAL).
FT DOMAIN 134 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 160 E (M5) (POTENTIAL).
FT DOMAIN 161 180 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 181 202 F (M5A) (POTENTIAL).
FT DOMAIN 203 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 211 232 G (M5B) (POTENTIAL).
FT DOMAIN 233 252 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 274 H (M6) (POTENTIAL).
FT DOMAIN 275 290 I (M7) (POTENTIAL).
FT TRANSMEM 291 309 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 310 340 J (M8) (POTENTIAL).
FT TRANSMEM 341 362 K (M9) (POTENTIAL).
FT DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 370 390 L, HYDROPHOBIC.
FT DOMAIN 391 405 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 406 426 M (M10) (POTENTIAL).
FT DOMAIN 427 435 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 436 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DOMAIN 457 834 CARBOHYD.
FT TRANSMEM 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 326 N-LINKED (GLCNAC. .) (POTENTIAL).
FT TRANSMEM 327 326 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 834 AA; 92907 MW; 3E7CE33D65DF36F7 CRC64;

Query Match 17.7%; Score 482.5; DB 1; Length 834;
Best Local Similarity 31.4%; Pred. No. 2.9e-24;
Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;

QY 48 VNESITALIIGCTGVVILLMTKQSSHL--FVSEDLFFIYLLPPIIFNAGFOVKKQF 105
DB 82 VPESALLIIGLVGGIV-----WAADHIASETLTPTVFFYLLPPVLDAGYFNPRLF 136
QY 106 FRNPMITLFCAGVCTMSFFITISAAIAISRMNIGILDVG--DFLAIGATFSATDSVCT 163
DB 137 FGNLGTILYAVGVTVWNAATTGSLYGVFLSGLMGDLQIGLDFLFGSLMAAADVPVAV 196
QY 164 LOVLNQ-DETPFLYSLVFGGVNDATSIYLFNALQNFDLV--HIDAADVLFKFLGNFFY 219
DB 197 LAVPEEVHVNELFIVFGESLLNDAVTVLYNVFESFVALGSDNVTVGDCVKGIVSFFV 256
QY 220 LFLSSTFLG-VFACLLSAYIYKLYICRHTDREVALMMLMAYLSYMLAELLDLSGLTV 278
DB 257 VSLGGTLVGVVFAFLS--LVTR--FTKHVRIIEPGFVFIIISYLSYLTSEMLSAILAI 312
QY 279 FFCGIVMSHYTWNVTSESSRVTKHAFATLSFAETFLYVGMDDLDEKWEFASDRPG 338
DB 313 TFCGICCKYVKANISQSATTVRYTMKMLASSAETIIFMFLGISAVNPFITWV----- 366
QY 339 KSTGISILLGLVIG--RAAFVPLSFLSNLTKKAPNEKITWRQOVVWAGLMRGAVS 396
DB 367 ---NTAPVLLTVFISYRAIGVGVVLOTWLLNRYRMVQLEPI---DQVLSYVGL-RGAVA 419
QY 397 IALAYNKFTSGHTQLHGNAI----MTSITIVLFSTWVF-QMNTKPLIR-LLLPASGH 450
DB 420 FALV-----VLDGDKVKENLKFVSTIIWVFTVIFQGLTIKPLVQWLKVRSEH 470
QY 451 PVTSEPPSPKSLH 463
DB 471 ---REPLNEKLH 480

RESULT 7
NAHL1_RABIT
ID NAHL1_RABIT STANDARD; PRT; 816 AA.
AC P23791.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE Sodium/hydrogen exchanger 1 (Na(+)/H(+)) exchanger 1) (NHE-1).
GN SLC9A1 OR NHE1
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE=ileal villus;
RX MEDLINE=91293066; PubMed=1712287;
RA Tse C.-M., Ma A.I., Yang W.W., Watson A.J.M., Levine S.,
RA Montrose M.H., Potter J., Sardet C., Pouyssegur J., Donowitz M.;
RT "Molecular cloning and expression of a cDNA encoding the rabbit ileal
RT villus cell basolateral membrane Na+/H+ exchanger.";
RL EMBO J. 10:1957-1967(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE=Heart muscle;
RX MEDLINE=92096447; PubMed=1661611;
RA Hildebrandt F., Pizzonia J.H., Reilly R.F., Reboucas N.A., Igarashi P.;
RA Sardet C., Pouyssegur J., Slayman C.W., Aronson P.S., Igarashi P.;
RT "Cloning, sequence, and tissue distribution of a rabbit renal Na+/H+
RT exchanger transcript.";
RL Biochim. Biophys. Acta 1129:105-108(1991).
RN [3]
RP SEQUENCE OF 472-816 FROM N.A.
RC STRAIN-New Zealand white; TISSUE=Heart muscle;
RX MEDLINE=91138752; PubMed=1704856;
RA Fliegel L., Sardet C., Pouyssegur J., Barr A.;
RT "Identification of the protein and cDNA of the cardiac Na+/H+
RT exchanger.";
RL FEBS Lett. 279:25-29(1991).
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: KIDNEY AND INTESTINE.
CC -1- PTM: PHOSPHORYLATED (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----
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CC -----
DR EMBL; X59935; CAA42558.1; -
DR EMBL; X61504; CAA43721.1; -
DR EMBL; X56536; CAA39881.1; -
DR PIR; S13926; S13926.
DR PIR; S16328; S16328.
DR InterPro; IPR000676; NaH_Exchange.
DR InterPro; IPR004709; NaH_exchange3.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR TIGRFAMs; TIGR00840; b_cpai; 1.
DR Transmembrane; Glycoprotein; Transport; Sodium transport;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 16 35 M1 (POTENTIAL).
FT DOMAIN 36 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 127 M2 (POTENTIAL).
FT DOMAIN 128 129 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 130 149 M3 (POTENTIAL).
FT DOMAIN 150 154 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 155 174 M4 (POTENTIAL).
FT DOMAIN 175 191 CYTOPLASMIC (POTENTIAL).

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Query Match      17.7%; Score 480.5; DB 1; Length 831;
Best Local Similarity 28.6%; Pred. No. 3.8e-24;
Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;

QY 22 VVSINLFVALLCACIV-LGHLLLENRWVNSITALLIGLCTGVVILLMTKGKSSHL--FV 78
Db 54 IIALWILVASLAKIVFHLSH--KVTSPVESALLVLGLVGLGIV-----WAADHIASET 106
QY 79 FSEDLFFIYLLPIIPNAGQVKKKOFFRNFMTITLFGAVGTMISPTTISIAAIAIFSRM 138
Db 107 LPTLFFFFYLLPIVLDAGYFMPNRLFFGNLGTILLYAVIGTILWNAATTGLSLUGVFLSG 166
QY 139 NIGTLVDG--DFLAIGAIFSDSVCTLOVLNQ--DETPELYSLVFGGVVNDATSVLFN 195
Db 167 LMGEKIGLGLDLFLGSLIAADVPVAVLAVFEVHVNEVLFITVFGESLLNDAVTVVLVN 226
QY 196 ALQNFDLVHIDAIV---VLKFLGNFFYFLSFTFLGV-FAGLLSAYIIRKLYIGRHSTDR 251
Db 227 VFESFVTLGGDAVTGDCVKGVISFPVSLGTLGVIFAFLLS--LVPR--FTKAVRII 282
QY 252 EVALMMLMAYLSYMLAEFLDLGILTVFCGIVMSHYTWHNVTESSRVTTKHAFATLSFI 311
Db 283 EPGFVFVISYLSYLTSEMLISAILAITFCGICCCQKVKANISEQSATTVRVTMKNLASG 342
QY 312 AETFLFYVGMADALDEKWEFASDRPKSGISGILLSLGLVLIG--RAAFVFPPLSFLSNTLT 369
Db 343 AETIFMFLGISAVDPVITW-----NTAFVLLTLVVISVRAIGVLOTWILNRY 393
QY 370 KAPNEKITWROOVVIMWAGLMRGAVSIALAYNKFTRSQHTQLHGNAIMITSTITVWLFS 429
Db 394 RMVQLETI---DOVVMYSVGL--RGAVAVLV---VLLDEKKVKKELNLPVSTLIVVFT 445
QY 430 TMVFGMTKPLRLILPASGHPVTSEPSPKSIH----SPLTSMQGSDELTSTNIVRPS 485
Db 446 VIFQELTKPLVQWLVKVRSE--QREPKLNEKLHGRADFHLISAIEDISGQIGHNLYRDK 503
QY 486 SLRMLLTKPTHTVHYWYRKED-----DALMR 511
Db 504 -----WSNFDKRLSKVLMLR 518

RESULT 9
NAH2_HUMAN
ID NAH2_HUMAN STANDARD; PRT; 812 AA.
AC Q9UB0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2).
GN SLC9A2 OR NHE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=99375108; PubMed=10444453;
RA Malakooti J., Dahdal R.Y., Schmidt L., Layden T.J., Dudeja P.K.,
RA Ramaswamy K.;
RT "Molecular cloning, tissue distribution, and functional expression of
RT the human Na(+)/H(+) exchanger NHE2."
RL Am. J. Physiol. 277:G383-G390(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hou S., Wohldmann P.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
CC COLONIC SODIUM ABSORPTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

```

-1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL INTESTINE.
 -1- PTM: PHOSPHORYLATED (POSSIBLE).
 -1- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 -1- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

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 EMBL: AF073299; AAD41635.1; -;
 EMBL: AC007239; AAF19248.1; -;
 GenBank: U00723; SLC9A2.
 MIM: 600530; -;
 InterPro: IPR000676; NaH_Exchange.
 InterPro: IPR004709; NaH_exchange3.
 Pfam: PF00999; NaH_Exchange; 1.
 PRINTS: PRO1084; NAHEXCHNGR.
 TIGRFAMs: TIGR00840; b_cpai; 1.
 Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 Multigene family; Phosphorylation.
 DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
 DOMAIN 14 33 A (M1) HYDROPHOBIC.
 DOMAIN 34 79 CYTOPLASMIC (POTENTIAL).
 DOMAIN 80 100 B (M2) HYDROPHOBIC.
 DOMAIN 101 106 CYTOPLASMIC (POTENTIAL).
 DOMAIN 107 127 C (M3) (POTENTIAL).
 DOMAIN 128 138 EXTRACELLULAR (POTENTIAL).
 DOMAIN 139 159 D (M4) (POTENTIAL).
 DOMAIN 160 168 E (M5) (POTENTIAL).
 DOMAIN 169 189 F (M5A) (POTENTIAL).
 DOMAIN 190 208 G (M5B) (POTENTIAL).
 DOMAIN 209 229 H (M6) (POTENTIAL).
 DOMAIN 230 236 I (M7) (POTENTIAL).
 DOMAIN 237 257 J (M8) (POTENTIAL).
 DOMAIN 258 277 K (M9) (POTENTIAL).
 DOMAIN 278 298 L, HYDROPHOBIC.
 DOMAIN 299 307 EXTRACELLULAR (POTENTIAL).
 DOMAIN 308 328 I (M7) (POTENTIAL).
 DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).
 DOMAIN 361 381 J (M8) (POTENTIAL).
 DOMAIN 382 391 CYTOPLASMIC (POTENTIAL).
 DOMAIN 392 412 K (M9) (POTENTIAL).
 DOMAIN 413 429 EXTRACELLULAR (POTENTIAL).
 DOMAIN 430 450 L, HYDROPHOBIC.
 DOMAIN 451 458 EXTRACELLULAR (POTENTIAL).
 DOMAIN 459 479 M13 (POTENTIAL).
 DOMAIN 480 812 CYTOPLASMIC (POTENTIAL).
 DOMAIN 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
 CARBOHYD CARBOHYD 350 350
 SEQUENCE 812 AA; 91519 MW; 17EE17DC3830D0A CRC64;
 Query Match 17.6%; Score 480; DB 1; Length 812;
 Best Local Similarity 27.3%; Pred. No. 4e-24;
 Matches 143; Conservative 98; Mismatches 203; Indels 80; Gaps 19;
 QY 16 TSDYASV---VSNLFVALLCACIVLHLLLE-NRWVNESITALLIGLCTGVVILLMTKG 71
 Db 72 TLDYPHVOIPETITLWLLSLAKLIGFHYHKLPTIVPESCLIMVGLLGGIIFGVDE- 130
 QY 72 KSHLFESEDFEFTYLLPPIIFNAGFOVKKQFRNEMTITLFCAGVTMTISFFITAA 131
 Db 131 KSPD--AMKTDVFFYLLPPIVLDAGYFMPTRPFENIGTIFWAVGTWNSIGIGVSL 188
 QY 132 IATFSRNIGTLDVG--DFLAIGAIFSDSVCTLOVL--NODETPFLYSLVFGGVNDA 188
 Db 189 FGICQIEAFGLSDITLLQNLFLGSLISAVDPVAVLAVFENIHNVEQLYLVFGESLLNDA 248

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC TISSUE=Stomach;
 RX MEDLINE=93280160; PubMed=7685026;
 RA Wang Z., Orłowski J., Shull G.E.;
 RT "Primary structure and functional expression of a novel
 RL gastrointestinal isoform of the rat Na/H exchanger.";
 RN J. Biol. Chem. 268:11925-11928(1993).
 [2]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC STRAIN=Sprague-Dawley; TISSUE=Small intestine;
 RX MEDLINE=93248205; PubMed=7683411;
 RA Collins J.F., Honda T., Knobel S., Bulus N.M., Conary J.,
 RT Dubois R., Ghishan F.K.;
 RL "Molecular cloning, sequencing, tissue distribution, and functional
 RT expression of a Na⁺/H⁺ exchanger (NHE-2)." ;
 RN Proc. Natl. Acad. Sci. U.S.A. 90:3938-3942(1993).
 [3]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE=Liver;
 RX MEDLINE=96129297; PubMed=8595899;
 RA Ghishan F.K., Knobel S.M., Summar M.;
 RT "Molecular cloning, sequencing, chromosomal localization, and tissue
 RL distribution of the human Na⁺/H⁺ exchanger (SLC9A2)." ;
 RN Genomics 30:25-30(1995).
 CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
 CC COLONIC SODIUM ABSORPTION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN SMALL INTESTINE, COLON, AND
 CC STOMACH, WITH MUCH LOWER LEVELS IN SKELETAL MUSCLE, KIDNEY, BRAIN,
 CC TESTIS, UTERUS, HEART, AND LUNG.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -!- CAUTION: REF.3 SEQUENCE WAS ORIGINALLY THOUGHT TO ORIGINATE FROM
 CC HUMAN.
 CC -----
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 CC -----
 DR EMBL; L11236; AAA72350.1; -;
 DR EMBL; L11004; AAA75406.1; -;
 DR EMBL; S81591; AAB36180.1; -;
 DR InterPro; IPR000676; NaH_Exchngr.
 DR InterPro; IPR004709; NaH_Exchngr.
 DR Pfam; PF00999; Na_H_Exchanger; 1.
 DR PRINTS; PR01084; NAHEXCHNGR.
 DR TIGRFAMs; TIGR00840; b_cpai; 1.
 DR Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation; Alternative splicing.
 FT DOMAIN 1 13
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 14 34
 FT A (M1) HYDROPHOBIC.
 FT DOMAIN 35 80
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 81 101
 FT B (M2) HYDROPHOBIC.
 FT DOMAIN 102 107
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 108 128
 FT C (M3) (POTENTIAL).
 FT DOMAIN 129 139
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 140 160
 FT D (M4) (POTENTIAL).
 FT DOMAIN 161 169
 FT CYTOPLASMIC (POTENTIAL).

TRANSMEM 170 190
 FT DOMAIN 191 209
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 210 230
 FT F (M5A) (POTENTIAL).
 FT DOMAIN 231 237
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 258
 FT G (M5B) (POTENTIAL).
 FT DOMAIN 259 278
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 279 299
 FT H (M6) (POTENTIAL).
 FT DOMAIN 300 308
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 309 329
 FT I (M7) (POTENTIAL).
 FT DOMAIN 330 361
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 362 382
 FT J (M8) (POTENTIAL).
 FT DOMAIN 383 392
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 393 413
 FT K (M9) (POTENTIAL).
 FT DOMAIN 414 430
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 431 451
 FT L, HYDROPHOBIC.
 FT TRANSMEM 452 459
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 460 480
 FT M13 (POTENTIAL).
 FT DOMAIN 481 813
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 351 351
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 1 116
 FT MISSING (IN SHORT ISOFORM).
 FT CONFLICT 504 504
 FT H -> HW (IN REF. 3).
 FT CONFLICT 610 616
 FT LYOIROR -> SUSNPPA (IN REF. 3).
 FT CONFLICT 742 742
 FT A -> P (IN REF. 3).
 FT CONFLICT 786 786
 FT V -> G (IN REF. 2).
 SQ SEQUENCE 813 AA; 29727267D7085845 CRC64;
 Query Match 17.6%; Score 479; DB 1; Length 813;
 Best Local Similarity 27.3%; Pred. No. 4.7e-24;
 Matches 143; Conservative 95; Mismatches 206; Indels 80; Gaps 19;
 QY 16 TSDYASV---VSNLFVALLCACIVLGLHLEE-NRWVNESITAIIGLCYGVVILLMTKG 71
 DB 73 TLDYPHVQIPFEITLWILLASLAKIGFHYKLPITVPESCILLIMVLLGGIIFGVDE- 131
 QY 72 KSHLFESEDLFFIYLLPIIFNAGFOVKKOFFRNFMTITILFGAVGTMISFTTISIAA 131
 DB 132 KSPD--AMKTVDFVLLPPIVDLDAGYFMPTRPFENLGTIFWYAVVGTWNIGIGLSL 189
 QY 132 IAIFSRMNTGLDVG--DFAIGAIFSATSDSVCTLOVL-NODETPFLYSLVFGGVVND 188
 DB 190 FGICQIEAFGLSDITLQNLFLGSLISAVDPVAVLAVFENIHVNEQLYILVFGESLLNDA 249
 QY 189 TSIVLFLNALQNF-DLVHIDAAVVVKELGNFFYFLFSLSTFLGVFAGLLSAY-----I 238
 DB 250 VTIVLYNLFKSCQMKTIQTVDFVAGIANFVVGIVGGVILGILLGFIAAFTTFTHNIRV 309
 QY 239 IKKLYIGRHSTREVALMMLAYLSYMLAELDLDSGLITVFFCGIVMSHTYHINVTESR 298
 DB 310 IEPLFV-----FLSYLSYITAEFMHLSGIMAITACAMTMNKYVEENVVSQKSY 357
 QY 299 VTKHAFATLSIAETFLFYVGMAL-DIEKWEFASDRPGKSGISGILLSIGLVLRGAA 357
 DB 358 TTIKYMKMLSSVSETLIFIPMGVSTVCKNHEMNA-----FVCFLLAFCLLWRAL 408
 QY 358 FVFPLSLNLTKKAPNEKITWROQVVIWAGLMRGAVSIALAY----NKFTRSHTOLH 413
 DB 409 GVFLVTQVINFRITP---LTFKDFIITAYGGL-RGAICFALVFLPATVFR----- 457
 QY 414 GNAMITSTITVLFSTWVEGMMTKPLRLLLPASGHPVTSSEPSKSLHSPLLTSMQGS 473
 DB 458 -KKLEITAAIVVFTVILGITIRPLVEFLDVKRSN--KKQAAVSEEHICRFFDHVK-T 513
 QY 474 DLESTNIVRPFSSRLMLLTKEPTHTVHYWR-----KFDDALMRPM 513
 DB 514 GIEDVCG-----HWGHNEWRDKKFKDDKYLRKL 542
 RESULT 12
 NAHL_MOUSE
 ID NAHL_MOUSE
 AC Q61165;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
Sodium/hydrogen exchanger 1 (Na⁺/H⁺) exchanger 1) (NHE-1).
SLC9A1 OR NHE1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=BAJB/C;
RA Dewey M.J., Bowman L.H.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -!- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
CC TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; U51112; AAA92976.1; -
DR MGD; MG1:102462; SLC9A1.
DR InterPro; IPR000676; NaH_Exchange.
DR InterPro; IPR004709; NaH_exchange3.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAEXCHNGR.
DR TIGRams; TIGR00840; b_cpai; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
KW Multigene family; Phosphorylation.
FT DOMAIN 1 12
FT DOMAIN 13 32
FT DOMAIN 33 105
FT DOMAIN 106 127
FT DOMAIN 128 130
FT TRANSMEM 131 150
FT DOMAIN 151 162
FT TRANSMEM 163 183
FT DOMAIN 184 188
FT TRANSMEM 189 210
FT DOMAIN 211 230
FT TRANSMEM 231 251
FT DOMAIN 252 260
FT TRANSMEM 261 282
FT DOMAIN 283 301
FT TRANSMEM 302 322
FT DOMAIN 323 336
FT TRANSMEM 337 357
FT DOMAIN 358 388
FT TRANSMEM 389 410
FT DOMAIN 411 416
FT TRANSMEM 417 438
FT DOMAIN 439 452
FT TRANSMEM 453 473
FT DOMAIN 474 482
FT TRANSMEM 483 503
FT DOMAIN 504 820
FT CARBOHYD 374 374
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 820 AA; 91467 MW; 0589C4D08DD348BE CRC64;

Query Match 17.6%; Score 479; DB 1; Length 820;

Best Local Similarity 29.1%; Pred. No. 4.7e-24;
Matches 147; Conservative 98; Mismatches 202; Indels 58; Gaps 19;
QY 18 DYASV---V--INFEVALLACIVLHLLLE-NEWNESITALIIGLCTGVVILLMKGKS 73
DB 99 DYHVRTPFISLWILLACIMKGFHVIPTISSIVPESCLLIIVVGLLVGLI----KGVG 154
QY 74 SHLFVSEDLFFIYLLPPIIFNAGFOVKKOFFERNFTITLFGAVGTIMISFFTTIS--IAA 131
DB 155 ETTPFLOSDFVFFLELLPIILDAGYFLPLRQFTENGLTILIFAVVGTLWNAFFLGLLYA 214
QY 132 IAFSRNIGTLDVGDFLAICAFSATSDVCTLOVLNQDE--TPFLSVLVEGEGVNDATS 190
DB 215 VCLVGGEOINNIGLDTLLFGSIIISAVDPVAVLAFPEEIHINELLHILVFGESILLDAVT 274
QY 191 IVLENALONF---DLVHDAAVLVKELGNFYLFLSSTFLGVFAGLLSAYIIKKLYIGH 247
DB 275 VVLYHLEEFASVDSVGI--SDIFLGLF--SFFVVALGVFVGVYVIAFTSR---FTSH 329
QY 248 STDREVALMMLMAYLSYMLAPLLDLSGLTVFFCGIVMSHYTHNVTESSRVTTKHAFAT 307
DB 330 IRVIEPLEFVLYSMAYLSAELFHLGIMALIASGVVMRPYVEANISHKSHITIKYFLKM 389
QY 308 LSFTIAETFLVYGVMDAL-DIEKWFASDRPGKISIGISILLGLVLIGRAAFVPLPFLS 366
DB 390 WSSVSETLIFIFLGVSTVAGSHOWNW-----TFVISTLL--FCLIAVLGLVLTWFI 440
QY 367 NLTKAPNEKITRQOVVIMWAGLARGAVSTALAYNKRTRSGHTQLHGNAMITSTIVV 426
DB 441 N---KFRIVKUTPKDQFIATYAGGL--RGAIAFSLGY--LLDKKHPMCD--LFLTAITVI 492
QY 427 LFTSMVGMCTKPIRLILLPASGHPVTSEPSKSLSPPLTSMQGSDELSTTNIVRPSS 486
DB 493 FFTVVGQMTIRPLVDLL-----AVKKQETKRSINEIHTQFLDHLLTGIEDIC---- 542
QY 487 LRMLLTKPTHTVHYWRKFDALMR 511
DB 543 -----GHYGHWHWK---DKLNR 556

RESULT 13
NAH5_RAT ID NAH5_RAT STANDARD; PRT; 898 AA.
AC Q920X2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 5 (Na⁺/H⁺) exchanger 5) (NHE-5).
GN SLC9A5 OR NHE5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=99134373; PubMed=9933642;
RA Attapahitaya S., Park K., Melvin J.E.;
RT "Molecular cloning and functional expression of a rat Na⁺/H⁺ exchanger
RT (NHE5) highly expressed in brain";
RL J. Biol. Chem. 274:4383-4388(1999);
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

RESULT 14					
NAHL_CRIGR	NAHL_CRIGR	STANDARD;	PRT;	822	AA.
ID	NAHL_CRIGR				
AC	P48761;				
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	15				

DE SLC9A1 or NHE1. Reports)
GN sodium/hydrogen exchanger 1 (Na⁽⁺⁾/H⁽⁺⁾ exchanger 1) (NHE-1).
OS Crictetus griseus (Chinese hamster).
OC Crictetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Crictetus.
OX NCBI_Taxid=10029;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=93192332; PubMed=8383540;
RX Counillon L., Pouyssegur J.;
RA "Biochemical sequence of the Chinese hamster Na⁺/H⁺ exchanger NHE1.";
RT Nucleic. Biophys., Acta 1172:343-345(1993).
RL -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
CC TRANSDUCTION.
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
CC
CC -!- SIMILARITY: BELONGS TO THE NA⁽⁺⁾/H⁽⁺⁾ EXCHANGER FAMILY.
CC
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA⁽⁺⁾/H⁽⁺⁾ EXCHANGERS VARY AMONG AUTHORS.
CC
CC -!- CAUTION:

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EMBL; X68970; CAA48771.1; ..
 InterPro; IPR000676; NaH_Exchange.
 InterPro; IPR004709; NaH_exchange?
 Pfam; PF00999; Na_H_Exchange; 1.
 PRINTS; PR01084; NAHEXCHNGR.
 TIGRFAMs; TIGR00840; b_cpai; 1.
 Trnsmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 Multigene family; Phosphorylation.
 DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 DOMAIN 13 32 A (M1) HYDROPHOBIC.
 DOMAIN 33 105 CYTOPLASMIC (POTENTIAL).
 DOMAIN 106 127 B (M2) HYDROPHOBIC.
 DOMAIN 128 130 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 131 150 C (M3) (POTENTIAL).
 DOMAIN 151 162 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 163 183 D (M4) (POTENTIAL).
 DOMAIN 184 188 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 189 210 E (M5) (POTENTIAL).
 DOMAIN 211 230 F (M5A) (POTENTIAL).
 TRANSMEM 231 251 G (M5B) (POTENTIAL).
 DOMAIN 252 260 H (M6) (POTENTIAL).
 TRANSMEM 261 282 I (M7) (POTENTIAL).
 DOMAIN 283 301 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 302 322 J (M8) (POTENTIAL).
 DOMAIN 323 336 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 337 357 I (M7) (POTENTIAL).
 DOMAIN 358 388 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 389 410 J (M8) (POTENTIAL).
 DOMAIN 411 416 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 417 416

TT	450	EXTRACELLULAR (POTENTIAL).	+
TD	452	EXTRACELLULAR (POTENTIAL).	+
TD	453	L ₁ HYDROPHOBIC.	

FT DOMAIN 474 482 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 483 503 M (M10) (POTENTIAL).
 FT DOMAIN 504 822 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 822 AA; 92003 MW; E97C1ACD4EB88DAA CRC64;
 Query Match 17.6%; Score 478; DB 1; Length 822;
 Best Local Similarity 28.7%; Pred. No. 5.5e-24;
 Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;
 QY 18 DYASV---VSNLNFVALLCACLIVLGHLEEE-NRWNESITALIIGLTCGVVILLMTKGS 73
 DB 99 DYLHRTPEISLWLLACLMKIGPHVPTISSIVPESCLLVGLLVGGGLI---KGVG 154
 QY 74 SHLFVSEDLFFIYLLPPIIFNAGQVKKOFFRNMFTITLFGAVGTWISFTTIS--IAA 131
 DB 155 ETPPFLQSDVFFELLPPIILDAGYFLPLRQFTENGLTILFVAVGTWLNFAFFLGGGLYA 214
 QY 132 IAIFSRMNTIGLDVGDFLAIGAIFATSVDCTLOVLNDE-TPFLYSLVFGGVNDATS 190
 DB 215 VCLVGEQINNTGLDITLFGSIISAVDPVAVVAVFEEIHINELLHILVFGESLNDATV 274
 QY 191 IVLFNALQ---NFDLVHDAVAVLFLGNFFFLSFLGAVGAGLISAYIIKKLYIGRH 247
 DB 275 VVLYHLFEFANYDSTGI--SDIFLGLF--SFFVVALGGVFGVGVVIAFTSR---FTSH 329
 QY 248 STDREVALMMLMAYLSYMLAELLDSGLTVFFCGIVMSHYTNHNVTESSRVTTKHAFAT 307
 DB 330 IRVIEPLFVFLSYMAYLSAEFLHLSGIMALIASGVMPVYVEANISHKSHHTTKIFLKM 389
 QY 308 LSFIAETFLFVGVGDAL--DIEKWEFASDPGKSGISISLLGLVLIGRAAFVFLPLSLS 366
 DB 390 WSSVSETLIFLGVSTVAGSHQWNN-----TFVISTLL--FCLIAVLGLVLTWFI 440
 QY 367 NLTKAPNEKITWROQVVTWAGLMRGAVSIALATNKFTRSGHTQIHGNAMITITIVV 426
 DB 441 N---KPRIVKTPKQFIAYGGL-REGAIFSLGY--LMDKKHFPMD--LFLTAITIVI 492
 QY 427 LFTSMVFGMTKPLIRLLPASGHPVTSBPSPKSLHSPLLTSMQGSDESNTNVRPSS 486
 DB 493 FTFVVGQMTIRPLVDLL-----AVKKQETKRSINEIEHTQFLDHLTLTGIEDIC--- 542
 QY 487 LRMLLTKPHTHYVYWRKEDDALMR 511
 DB 543 -----GHYGHGHMK-----DKLNR 556
 PRT; 817 AA.
 RESULT 15
 ID NAHL_BOVIN STANDARD; PRT; 817 AA.
 AC Q28036;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/hydrogen exchanger 1 (Na(+)/H(+)) exchanger 1 (NHE-1).
 GN SLC9A1 OR NHE1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Zhu H., Zhang Q., Zhang X., Liu W., Trumbly R.J., Garlid K.D.,
 RA Sun X.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
 CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
 CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
 CC SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
 CC TRANSDUCTION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
 CC -!- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
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 CC -----
 CC EMBL: U49432; AAA91483.1; --
 DR InterPro: IPR000676; Nahl_Exchange.
 DR InterPro: IPR004709; Nahl_Exchange3.
 DR Pfam: PF00999; Na_H_Exchange; 1.
 DR PRINTS: PR01084; NAHEXCHNGR.
 DR TIGRFAMs: TIGR00840; b_cpah; 1.
 KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation.
 DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 16 35 M1 (POTENTIAL).
 FT DOMAIN 36 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 127 M2 (POTENTIAL).
 FT DOMAIN 128 129 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 130 149 M3 (POTENTIAL).
 FT DOMAIN 150 154 M4 (POTENTIAL).
 FT TRANSMEM 155 174 M5 (POTENTIAL).
 FT DOMAIN 175 191 M6 (POTENTIAL).
 FT TRANSMEM 192 211 M7 (POTENTIAL).
 FT DOMAIN 212 227 M8 (POTENTIAL).
 FT TRANSMEM 228 247 M9 (POTENTIAL).
 FT DOMAIN 248 256 M10 (POTENTIAL).
 FT TRANSMEM 257 276 M11 (POTENTIAL).
 FT DOMAIN 277 294 M12 (POTENTIAL).
 FT TRANSMEM 295 315 M13 (POTENTIAL).
 FT DOMAIN 316 338 M14 (POTENTIAL).
 FT TRANSMEM 339 358 M15 (POTENTIAL).
 FT DOMAIN 359 386 M16 (POTENTIAL).
 FT TRANSMEM 387 406 M17 (POTENTIAL).
 FT DOMAIN 407 410 M18 (POTENTIAL).
 FT TRANSMEM 411 430 M19 (POTENTIAL).
 FT DOMAIN 431 480 M20 (POTENTIAL).
 FT TRANSMEM 481 500 M21 (POTENTIAL).
 FT DOMAIN 501 817 M22 (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 370 370 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 817 AA; 91017 MW; 6617E99D3B012920 CRC64;
 Query Match 17.5%; Score 476; DB 1; Length 817;
 Best Local Similarity 28.8%; Pred. No. 7.4e-24;
 Matches 146; Conservative 98; Mismatches 201; Indels 62; Gaps 19;
 QY 18 DYASV---VSNLNFVALLCACLIVLGHLEEE-NRWNESITALIIGLTCGVVILLMTKGS 73
 DB 95 DYQHVRIPEFETALWLLACLMKIGPHVPTISSIVPESCLLVGLLVGGGLI---KGVG 150
 QY 74 SHLFVSEDLFFIYLLPPIIFNAGQVKKOFFRNMFTITLFGAVGTWISFTTIS--IAA 131
 DB 151 ETPPILQSEVFFLPLPPIILDAGYFLPLRQFTENGLTILFVAVGTWLNFAFFLGGGLYA 210
 QY 132 IAIFSRMNTIGLDVGDFLAIGAIFATSVDCTLOVLNDE-TPFLYSLVFGGVNDATS 190
 DB 211 VCLVGEQINNTGLLENLFGSIISAVDPVAVVAVFEEIHINELLHILVFGESLNDATV 270
 QY 191 IVLFNALQ---NFDLVHDAVAVLFLGNFFFLSFLGAVGAGLISAYIIKKLYIGRH 247
 DB 271 VVLYHLFEFANYDRVGI--VDIILGLF--SFFVVALGGVFGVGVVIAFTSR---FTSH 325
 QY 248 STDREVALMMLMAYLSYMLAELLDSGLTVFFCGIVMSHYTNHNVTESSRVTTKHAFAT 307

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Db 326 IRVIEPLFVFLYSMAYLSAELFHLJSGIMALTASGVYMRPYVEANISHKSHTTIKYFLKM 385
QY 308 LSFIAETFLFLYVGMALDIE---KWEFASDRPGKSIGISSILGVLIGRAAFVPEPLSF 364
Db 386 WSSVSETLFIELGVSTVAGSHHWNWTFV-----ISTLL--FCLLARVLGVLGLTW 434
QY 365 LSNLTKKAPNEKITWRQOVVIWAGLMRGAVSIALAYNNKFTRSHTQLHGNAMITSTYT 424
Db 435 FIN---KFRIVKLTPKDQFIAYGGL-RGAIAFSLGY--LLDKKHFPMD--LFLTAIIT 486
QY 425 VVLESTWVFGMMTKPLIRLLLPASGHPVISEPSSPKSLHSPLLTSMQGSDDLESTTNIVRP 484
Db 487 VIFFTFVOGMTIRPLVDLL-----AVKKKOETKRSINEEHTQFLDHLTLTGIEDIC-- 538
QY 485 SSLRMLLTAKPTHVHYWYWKFDLALMR 511
Db 539 -----GHYGHHWK---DKLNR 552

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Search completed: March 26, 2003, 18:53:06
Job time : 34 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:49:39 ; Search time 38 Seconds
(without alignments)
2900.926 Million cell updates/sec

Title: US-09-888-035A-2
Perfect score: 2722
Sequence: 1 MGMEVAARLGALYTTSDYA.....GRGFVPFSPCSPTQSHGGR 535

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2722	100.0	535	10	Q9SXJ8		Q9sxj8 oryza sativ
2	2105.5	77.4	555	10	Q9FZM0		Q9fzn0 atriplex gm
3	2103.5	77.3	540	10	Q94LX5		Q94lx5 petunia hyb
4	2095.5	77.0	553	10	Q94LX4		Q94lx4 nierenbergi
5	2080	76.4	546	10	Q9CAW6		Q9caw6 arabidopsis
6	2065.5	75.9	542	10	Q94IE0		Q94ie0 ipomoea tri
7	2055.5	75.5	542	10	Q9FEB3		Q9feb3 pharbitis n
8	2054.5	75.5	556	10	Q94K25		Q94k25 sueda mari
9	2043	75.1	542	10	Q9ARH6		Q9arh6 citrus para
10	2023.5	74.3	538	10	Q9ZPK3		Q9zpk3 arabidopsis
11	1966	72.2	555	10	Q94LX3		Q94lx3 torenia hyb
12	1931	70.9	552	10	Q9SQU0		Q9squ0 arabidopsis
13	1921.5	70.6	546	10	Q94BM4		Q94bm4 triticum ae
14	1879	69.0	534	10	Q93YH2		Q93yh2 lycopersico
15	1698.5	62.4	457	10	O04655		O04655 arabidopsis
16	1529	56.2	529	10	Q9FJ63		Q9fj63 arabidopsis

17	1529	56.2	529	10	Q8S397		Q8s397 arabidopsis
18	1356	49.8	295	10	Q94BM3		Q94bm3 triticum ae
19	619	22.7	576	11	Q8R4D1		Q8r4d1 mus musculu
20	595.5	21.9	561	5	Q9XZM4		Q9xzm4 drosophila
21	595.5	21.9	649	5	Q9VPJ1		Q9vpj1 drosophila
22	592.5	21.8	649	5	Q8SZX8		Q8szx8 drosophila
23	579.5	21.3	611	5	Q8T5R7		Q8t5r7 caenorhabdi
24	579.5	21.3	630	5	Q8T5R8		Q8t5r8 caenorhabdi
25	569	20.9	687	5	Q9U624		Q9u624 drosophila
26	567.5	20.8	629	5	Q20944		Q20944 caenorhabdi
27	565	20.8	727	5	Q9VM99		Q9vm99 drosophila
28	564.5	20.7	655	5	Q8T5R3		Q8t5r3 caenorhabdi
29	564.5	20.7	681	5	Q8T5R4		Q8t5r4 caenorhabdi
30	564.5	20.7	703	5	Q9XW14		Q9xw14 caenorhabdi
31	558.5	20.5	517	10	Q8S396		Q8s396 arabidopsis
32	553	20.3	725	4	Q96T83		Q96t83 homo sapien
33	552	20.3	569	3	O13726		O13726 schizosacch
34	551	20.2	531	10	Q93YH1		Q93yh1 lycopersico
35	546	20.1	525	10	Q8S395		Q8s395 arabidopsis
36	545	20.0	535	10	Q8RW06		Q8rwu6 arabidopsis
37	533	19.6	140	10	O91KH5		O91kh5 mesembryant
38	528	19.4	153	10	O9LKH6		O9lkh6 mesembryant
39	513	18.8	106	10	Q9ATZ9		Q9atz9 zea mays (m
40	497.5	18.3	437	4	Q9Y507		Q9y507 homo sapien
41	488.5	17.9	560	3	Q9HEX3		Q9hex3 pneumocysti
42	475.5	17.5	518	5	Q9VIF9		Q9vif9 drosophila
43	475.5	17.5	582	5	Q8WPH4		Q8wph4 drosophila
44	467	17.2	1203	5	Q9NGZ4		Q9ngz4 drosophila
45	459.5	16.9	1179	5	Q9NCQ0		Q9ncq0 aedes aegyp

ALIGNMENTS

RESULT 1

Q9SXJ8	ID	Q9SXJ8	PRELIMINARY:	PRT;	535 AA.
AC	Q9SXJ8;				
DT	01-MAY-2000	(TrEMBLrel. 13, Created)			
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DE	OSNHX1	protein.			
GN	OSNHX1				
OS	Oryza sativa (Rice).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Ehrhartoideae; Oryzeae; Oryza.				
OX	NCBI_TaxID=4530;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	STRAIN=CV. NIPPONBARE;				
RX	MEDLINE=93326147; PubMed=10395929;				
RA	Fukuda A., Nakamura A., Tanaka Y.;				
RT	"Molecular cloning and expression of the Na+/H+ exchanger gene in Oryza sativa.";				
RL	Biochim. Biophys. Acta 1446:149-155(1999).				
DR	EMBL: AB021878; BAA83337.1; .				
DR	InterPro: IPR004709; NaH_exchang3.				
DR	InterPro: IPR000676; NaH_exchangr.				
DR	Pfam: PF00999; Na_H_Exchange; 1.				
DR	PRINTS: PR01084; NAHEXCHNGR.				
DR	TIGRFAMS: TIGR00840; b_cpai; 1.				
SQ	SEQUENCE 535 AA; 59070 MW; 6BCADB29B131976 CRC64;				

Query Match	100.0%;	Score 2722;	DB 10;	Length 535;
Best Local Similarity	100.0%;	Pred. No. 7.4e-193;		
Matches 535;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	MGMEVAARLGALYTTSDYASVWSINLFVALLCACIVLGHLLLEENRWVNESITALIIGLC	60	
Db	1	MGMEVAARLGALYTTSDYASVWSINLFVALLCACIVLGHLLLEENRWVNESITALIIGLC	60	
Oy	61	TGCVILLMTKGKSSHLVFSEDLFFIYLLPPIIFNAGFOVKKOFFRNFMTITLFGAVGT	120	

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Db 61 TGVVILLMTKSSHLVFESEDLFFIYLLPPIIFNAGFQVKKQFRFNMFTTLFGAVGT 120
QY 121 MISFETISIAAIAIFSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVNODETPFLYSLVLF 180
Db 121 MISFETISIAAIAIFSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVNODETPFLYSLVLF 180
QY 181 GEGVNDATSIIVFNALONFOLVHIDAADVVLKFLGNFFYFLFUSSTFLGVFAGLLSAYIIK 240
Db 181 GEGVNDATSIIVFNALONFOLVHIDAADVVLKFLGNFFYFLFUSSTFLGVFAGLLSAYIIK 240
QY 241 KLYIGRSTDRVALMMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTHWNVTSSRYT 300
Db 241 KLYIGRSTDRVALMMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTHWNVTSSRYT 300
QY 301 TKHAPATLSFAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVF 360
Db 301 TKHAPATLSFAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVF 360
QY 361 PLSFSLNLTKKAPNEKITWROOVVIWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMIT 420
Db 361 PLSFSLNLTKKAPNEKITWROOVVIWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMIT 420
QY 421 STITVLFSTVFGMNTKPLIRLLPASGHVPTSPSPKSLHSPPLTSMOGSDLESTTN 480
Db 421 STITVLFSTVFGMNTKPLIRLLPASGHVPTSPSPKSLHSPPLTSMOGSDLESTTN 480
QY 481 IVRSSRLMLTKPHTVHYWYWRKFDDALMRPFGRGVFPFSPGSPTEQSHGGR 535
Db 481 IVRSSRLMLTKPHTVHYWYWRKFDDALMRPFGRGVFPFSPGSPTEQSHGGR 535

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RESULT 2

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Q9FZNO PRELIMINARY; PRT; 555 AA.
AC Q9FZNO;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Na/H antiporter Nhx1.
GN AGNHX1.
OS Atriplex gmelini.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Atriplex.
OX NCBI_TaxID=118074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21330247; PubMed=11437248;
RA Hamada A., Shono M., Xia T., Ohta M., Hayashi Y., Tanaka A.,
RA Hayakawa T.
RT "Isolation and characterization of a Na+/H+ antiporter gene from the
RT halophyte Atriplex gmelini."
RL Plant Mol. Biol. 46:35-42(2001).
DR EMBL; AB038492; BAB11940.1; -.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 555 AA; 61504 MW; ACD5ED45FF3D398A CRC64;

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Query Match 77.4%; Score 2105.5; DB 10; Length 555;
 Best Local Similarity 76.8%; Pred. No. 2.3e-147;
 Matches 410; Conservative 53; Mismatches 61; Indels 15; Gaps 4;

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QY 7 AARLGALYTTSDXASVSVINLFAVALLCACIVLGHLLERNRWNESITALIIGLCTGVVIL 66
Db 10 SGRKMDL-TTSDRASVSMNLFAVALLCCIVIGHLLERNRWNESITALIIGLCTGVVIL 68
QY 67 LMTKGSLSHLVFESEDLFFIYLLPPIIFNAGFQVKKQFRFNMFTTLFGAVGTMSIFFT 126
Db 69 LISGGKSHLLVFESEDLFFIYLLPPIIFNAGFQVKKQFRFNMFTTLFGAVGTMSIFFT 128

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QY 127 ISTAIAIAIFSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVNODETPFLYSLVFGGVVN 186
Db 129 ISUGALSIFKLDIGTLEADYLAIGAIPAADVSVCTLOVNODETPFLYSLVFGGVVN 188
QY 187 DATSIIVFNALONFOLVHIDAADVVLKFLGNFFYFLFUSSTFLGVFAGLLSAYIIKKLYIGR 246
Db 189 DATSVVLENAIQSFDLTRIDHRIALQFMGNFLYLFIASTILGFTGLLSAYIIKKLYFGR 248
QY 247 HSTDREVALMMLMAYLSYMLAEELDLGSLTVFFCGIVMSHYTHWNVTSSRYTKHAPA 306
Db 249 HSTDREVALMMLMAYLSYMLAEELFYLSGILTVFFCGIVMSHYTHWNVTSSRYTKHAPA 308
QY 307 TLSFIAETFLFYVGMALDIEKWEFASDRPGKSGISILLGLVLIGRAAFVFLSPLS 366
Db 309 TLSFVAEVFLFYVGMALDIEKWEFASDRPGKSGISIVAVSILLGLVWGRAAFVFLSWM 368
QY 367 NLTKAPNEKITWROOVVIWAGLMRGAVSIALAYNKFTTRSGHTOLHGNAMITITVYV 426
Db 369 NFAKKSQSEKVTNFQOIVIWAGLMRGAVSIALAYNQFTTRSGHTOLRGNAMITITISVV 428
QY 427 LFTSMVFGMNTKPLIRLLPASGHVPTSPSPKSLHSPPLTSMOGSDL----- 475
Db 429 LFTSMVFGMNTKPLIRLLPASGHVPTSPSPKSLHSPPLTSMOGSDL----- 475
QY 476 ESTT---NIVRPSSRLMLTKPHTVHYWYWRKFDDALMRPFGRGVFPFSPGSPTEQS 531
Db 489 EDTTEPRIVRPSSRLMLLNAPHTVHYWYWRKFDDSEMRPFGRGVFPFSPGSPTEQS 547

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RESULT 3

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Q94LX5 PRELIMINARY; PRT; 540 AA.
AC Q94LX5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Na H-antiporter.
GN PHUPRPLE.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RA Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;
RT "Plant Na-H antiporter."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051817; BAB56105.1; -.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR000676; NaH_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 540 AA; 59510 MW; BCE2740F275E896A CRC64;

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Query Match 77.3%; Score 2103.5; DB 10; Length 540;
 Best Local Similarity 77.4%; Pred. No. 3.2e-147;
 Matches 404; Conservative 53; Mismatches 62; Indels 3; Gaps 1;

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QY 15 TTSYASVSVINLFAVALLCACIVLGHLLERNRWNESITALIIGLCTGVVILMTKGSS 74
Db 16 STDSHQSVSVINLFAVALLCACIVLGHLLERNRWNESITALVIGSCTGIVILLISGGKS 75
QY 75 HLFVSEDLFFIYLLPPIIFNAGFQVKKQFRFNMFTTLFGAVGTMSIFFTISAAAI 134
Db 76 HILVSEDLFFIYLLPPIIFNAGFQVKKQFRFNMFTTLFGALGTLLISFIISLGAIGI 135
QY 135 FSRMNICTLDVGDFLAIGAIFSAITSDSVCTLOVNODETPFLYSLVFGGVNDATSIIVLF 194
Db 136 FKKMNGISLEIGDYLAIGAIFSAITSDSVCTLOVNODETPFLYSLVFGGVNDATSVVLF 195
QY 195 NALONFOLVHIDAADVVLKFLGNFFYFLFUSSTFLGVFAGLLSAYIIKKLYIGRHTDREVA 254

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Db 196 NAIONFDLSDHDTCKAMELVGNFLYLFPASSTALGVAAGLLSAYIIKKLYFGRHSTDREVA 255
Qy 255 LMLMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAET 314
Db 256 IMILMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAEI 315
Qy 315 FFLYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 374
Db 316 FFLYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 375
Qy 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTSRGHTOLHGNAMITSTITVVLFSFVFG 434
Db 376 AKISFNQOVTIWWAGLMRGAVSMALAYNQFTRGHTQLRANAMITSTITVVLFSFVFG 435
Qy 435 MMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMQGSDLESTTNIVRPSLRMLL 491
Db 436 LMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMQGSDLESTTNIVRPSLRMLL 495
Qy 492 TKPHTVHYWYRKFDALMRPFGGRGVFPSPGSPTEQSHG 533
Db 496 STPSTVHYWYRKFDALMRPFGGRGVFPSPGSPTEQSHG 537

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RESULT 4
Q94LX4
ID Q94LX4 PRELIMINARY; PRT: 553 AA.
AC Q94LX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Na H-antiporator.
CN NHPURPLE.
OS Nierembergia caerulea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nierembergia.
OX NCBI_TaxID=144865;
RN [1]
RP SEQUENCE FROM N.A.
RA Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;
RT "Plant Na-H antiporator."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB051818; BAB56106.1;
DR InterPro: IPR001179; FKBP_Pptase.
DR InterPro: IPR004709; NaH_exchng3.
DR InterPro: IPR000676; NaH_exchng1.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR TIGRFAMs: TIGR00840; b_Cpal; 1.
DR PROSITE: PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ SEQUENCE 553 AA; 61119 MW; 9F2B47A49D7AB2CC CRC64;

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Query Match 77.0%; Score 2095.5; DB 10; Length 553;
Best Local Similarity 77.8%; Pred. No. 1.3e-146;
Matches 403; Conservative 49; Mismatches 63; Indels 3; Gaps 1;

Qy 15 TTSDYASVYVNLFFVALLCACIVGLHLEENRWVESITALLIGCTGWTLLMTKGSS 74
Db 16 TTSDHQSVVSNLFFVALLCACIVGLHLEENRWVESITALLIGCTGWTLLMTKGSS 75
Qy 75 HLFVSEDLFFTYLLPPIIFNAGFOVKKQFFRNFTITLFGAVGTMTSFTTISTATAI 134
Db 76 HLFVSEDLFFTYLLPPIIFNAGFOVKKQFFRNFTITLFGAVGTMTSFTTISTATAI 135
Qy 135 FSRMNGITLVDGFLAIGAFISATSVCTQLVNODETPFLYSLVFGGVNDATSVILF 194
Db 136 FKMDIGHLEIGDYLGAIFAATSVCTQLVNODETPFLYSLVFGGVNDATSVILF 195
Qy 195 NALQNFDLVHDAVAAVFNFFFLSFLSFLGAGLLSAYIIKKLYFGRHSTDREVA 254
Db 196 NALQNFDLVHDAVAAVFNFFFLSFLSFLGAGLLSAYIIKKLYFGRHSTDREVA 255
Qy 255 LMLMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAET 314

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Db 256 IMILMAYLSYMLAEILLDLSGLTAVFFCGIVMNSHYTHWNTVTESSRVTTKHAFATLSFIAEI 315
Qy 315 FFLYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 374
Db 316 FFLYVGMALDIEKWEFASDRPCKSGISILLGLVLIGRAAFVFPFLSFLSNLTKKAPN 375
Qy 375 EKITWROQVVIWAGLMRGAVSIALAYNKFTSRGHTOLHGNAMITSTITVVLFSFVFG 434
Db 376 AKISFNQOVTIWWAGLMRGAVSMALAYNQFTRGHTQLRANAMITSTITVVLFSFVFG 435
Qy 435 MMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMQGSDLESTTNIVRPSLRMLL 491
Db 436 LMTKPLIRLLPASGH---PVTSEPSKSLHSPILTSMQGSDLESTTNIVRPSLRMLL 495
Qy 492 TKPHTVHYWYRKFDALMRPFGGRGVFPSPGSPTEQSHG 529
Db 496 STPSTVHYWYRKFDALMRPFGGRGVFPSPGSPTEQSHG 533

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RESULT 5
Q9CAW6
ID Q9CAW6 PRELIMINARY; PRT: 546 AA.
AC Q9CAW6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative sodium proton exchanger (Na+/H+ exchanger 2).
GN T9J14.2 OR NHX2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Cholsen N., Artiguenave F., Robert C., Brotter P.,
RA Wacker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Otterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Millscher J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Iwasawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana."
RL Nature 408:820-822(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yokoi S., Quintero F.J., Cubero B., Ruiz T., Bressan R.A.,
RA Hasegawa P.M., Pardo J.M.;
RT "Differential expression and function of Arabidopsis thaliana NHX Na+/H+ antiporters in the salt stress response."

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... increasing the frequency and/or exchange and flower coloration.

[2]


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RP SEQUENCE FROM N.A.
RC STRAIN-PR-R; TISSUE-LEAF;
RX MEDLINE=21276661; PubMed=11382810;
RA Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N.,
RA Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.;
RT "Genes Encoding the Vacuolar Na+/H+ Exchanger and Flower Coloration.";
RL Plant Cell Physiol. 42:451-461(2001).
DR EMBL; AB033990; BAB16381.1; -
DR EMBL; AB033989; BAB16380.1; -
DR EMBL; AB05062; BAB60899.1; -
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR004709; Nah_Exchange3.
DR InterPro; IPR000676; Nah_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR TIGRFAMS; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
SQ SEQUENCE 542 AA; 59973 MW; 4B47FDE0401A191 CRC64;

Query Match 75.5%; Score 2055.5; DB 10; Length 542;
Best Local Similarity 76.4%; Pred. No. 1.4e-143;
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;

QY 16 TSDASVVSINLFAVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGKSSH 75
DB 16 TSDASVVSINLFAVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGKSSH 75

QY 76 LFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAIAIF 135
DB 76 LFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAIAIF 135

QY 136 SRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVNODETPFLYSLVFGGVNDATSVILFN 195
DB 136 SRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVNODETPFLYSLVFGGVNDATSVILFN 195

QY 196 ALQNFDLVHDAVVKFLGHNFFFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDEVAL 255
DB 196 ALQNFDLVHDAVVKFLGHNFFFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDEVAL 255

QY 256 MMLMAYLSYMAELDLGSLITVFCGIVMSHYTHWNVTSSRVTTKHAFTLSFIAETP 315
DB 256 MMLMAYLSYMAELDLGSLITVFCGIVMSHYTHWNVTSSRVTTKHAFTLSFIAETP 315

QY 316 LFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTAKPNE 375
DB 316 LFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTAKPNE 375

QY 376 KITRQVVVIMWAGLRGAVSTALAYNKRFTSGHTQLHGNAMITSTITVVLFSTVFGM 435
DB 376 KITRQVVVIMWAGLRGAVSTALAYNKRFTSGHTQLHGNAMITSTITVVLFSTVFGM 435

QY 436 MTKPLIRLLP-----ASGHP--VTSEPPSPKSLHSPLLTSMQSDLESTT--NIVRPSS 486
DB 436 MTKPLIRLLP-----ASGHP--VTSEPPSPKSLHSPLLTSMQSDLESTT--NIVRPSS 486

QY 487 LRMLLTKPTHVHYVYWRKFDALMRPMFGGRGVFPSPGSPTEQS 531
DB 487 LRMLLTKPTHVHYVYWRKFDALMRPMFGGRGVFPSPGSPTEQS 531

QY 496 LRMLLTKPTHVHYVYWRKFDALMRPMFGGRGVFPSPGSPTEQS 540
DB 496 LRMLLTKPTHVHYVYWRKFDALMRPMFGGRGVFPSPGSPTEQS 540

RESULT 8
Q94K25 ID Q94K25 PRELIMINARY; PRT; 556 AA.
AC Q94K25;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Na+/H+ antiporter.
OS Suaeda maritima subsp. salsa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Suaeda.
OX NCBI_TaxID=126914;
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RP SEQUENCE FROM N.A.
RA Zhang H., Zhang Q., Ma X.;
RT "Na+/H+ antiporter in Suaeda salsa.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370358; AAK53432.1; -
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR004709; Nah_Exchange3.
DR InterPro; IPR000676; Nah_Exchange.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMS; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
SQ SEQUENCE 556 AA; 61672 MW; DDF6AB696647D48E CRC64;

Query Match 75.5%; Score 2054.5; DB 10; Length 556;
Best Local Similarity 74.2%; Pred. No. 1.4e-143;
Matches 395; Conservative 56; Mismatches 68; Indels 13; Gaps 2;

QY 13 LYTTSDYASVVSINLFAVALLCACIVLGHLLLEENRWNESITALIIGLCTGVVILLTKGK 72
DB 15 MVSTSDHASVVSNNLFAVALLRGCVIVGHLLLEENRWNESITALIIGLSTGIIILLISGGK 74

QY 73 SSHLFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAI 132
DB 75 SSHLFVSEDLFFIYLLPPIIFNAGQVKKQFFRNFMITLFGAVGTMTISFFTTISAAI 134

QY 133 AIFSRMNTIGTLDVGDFLAIGAIFSATDSVCTLOVNODETPFLYSLVFGGVNDATSVI 192
DB 135 AIFOKMDIGSLELGLDLAIGAIFATDSVCTLOVNODETPLLYSLVFGGVNDATSVV 194

QY 193 LFNALQNFDLVHDAVVKFLGHNFFFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDE 252
DB 195 LFNALQNFDLTHDHTAFQFNGNLYLFFASTLLGAVTGLLSAYIVTKLYFGRHSTDE 254

QY 253 VALMMLMAYLSYMAELDLGSLITVFCGIVMSHYTHWNVTSSRVTTKHAFTLSFIA 312
DB 255 VALMMLMAYLSYMAELFLYSLGILTVFCGIVMSHYTHWNVTSSRVTTKHAFTLSFVA 314

QY 313 ETFLYVGMALDIEKWEFASDRPKSIGISILLGLVLGIRAAFPPLSFLSNLTAKKA 372
DB 315 EIFLFLYVGMALDIEKWRVDSGPGSVAVSSILLGHVWGRAAFVFPFAFLMNLSSKS 374

QY 373 PNEKITRQVVVIMWAGLRGAVSIALAYNKRFTSGHTQLHGNAMITSTITVVLFSTV 432
DB 375 NSEKVTENQOQIVIMWAGLRGAVSVALAYNQFSRSGHTQLRGNAMITSTITVVLFSTV 434

QY 433 FGMATKPLIRLLP-----PVTSEPPSPKSLHSPLLTSMQSDLESTN----- 480
DB 435 FGLTKPLIRLLP-----PVTSEPPSPKSLHSPLLTSMQSDLESTN----- 480

QY 481 -IVRPSSLRMLTKPTHVHYVYWRKFDALMRPMFGGRGVFPSPGSPTEQS 531
DB 495 TIARPTSLRMLLNAPTHTVHYVYWRKFDALMRPMFGGRGVFPSPGSPTEQS 546

RESULT 9
Q9ARH6 ID Q9ARH6 PRELIMINARY; PRT; 542 AA.
AC Q9ARH6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Sodium/proton exchanger.
OS Citrus paradisi (Grapefruit).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=37656;

RP SEQUENCE FROM N.A.
RC TISSUE-PEEL;
RA Porat R., Lurie S., Povancello D.;
RT "A heat treatment induced the transcription of a sodium proton
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OC Torenia.
OX NCBI_TaxID=75807;
RN [1]
RP SEQUENCE FROM N.A.
RA Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;
RT "Plant Na-H antiporter."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051819; BAB56107.1; .
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR004709; NaH_exchng.
DR InterPro; IPR000676; NaH_exchng.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRfams; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
SQ SEQUENCE 555 AA; 61315 MW; FEF9556E029B3983 CRC64;

Query Match 72.2%; Score 1966; DB 10; Length 555;
Best Local Similarity 71.3%; Pred. No. 4.6e-137;
Matches 390; Conservative 55; Mismatches 84; Indels 18; Gaps 5;

QY 1 MGMEVAAARLGAALYTTSDYASVSNLFLVALLCACIVLGHLLLEENRWVNESITALI 56
   ||| :||: | :| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGFESVILKAASETNLW-SSGHGVAITLFLVLLCTIVLGHLLLEENRWVNESITALI 59

QY 57 IGLCTGVVILLMTGKSHLFESEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFG 116
   ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 IGLATGVILLISGGKSHLFESEDLFFIYALPPIIFNAGFQVKKKOFFRNFMTIMFG 119

QY 117 AVGTWISFTTISIAAIAIFSRNICTLDVDFLAIGAFSATDSVCTLOVLNQDETPLY 176
   ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 AVGTLLISFTIISLGTIAFFPKNM-RLGVGDYLAIGAFSATDSVCTLOVLNQDETPLY 178

QY 177 SLVFGGVNDATSIVLNALQNFDLVHDAAVLKFGLNFFYFLSLSTFLGVFAGLLSA 236
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 SLVFGGVNDATSIVLNFAVQNFDPHMTAKAFELVGNFFYLPATSTVLGVLGLLSA 238

QY 237 YIIKLYIGRSTDEVALMMLMAYLSYMLAELDLGILTVFFCGIVMSHYTHNVTES 296
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 YIIKLYIGRSTDEVALMMLMAYLSYMLAELDLGILTVFFCGIVMSHYTHNVTEN 298

QY 297 SVRTTKHATLSFAETFLFYVGMADLDIEKWFASFADRPCKSIGISILLGLVIGRA 356
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 SVRTTKHATLSFAETFLFYVGMADLDIEKWFASFADRPCKSIGISILLGLVIGRA 358

QY 357 AFVPLSLSLNLTKKAPNEKITRQOVVWAGLARGAVSIALAYNKTRSGHTOLHNA 416
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 AFVPLSLSLNLTKKAPNEKITRQOVVWAGLARGAVSIALAYNKTRSGHTOLHNA 418

QY 417 IMTSTITVTLFSTWVFGMTKPLIRLLPAS--GHPVTSESPSPKSLHSPL----- 466
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 IFITSTITVTLFSTWVFGMTKPLIRLLPAS--GHPVTSESPSPKSLHSPL----- 478

QY 467 --LTSQGSLESTTNVVRPSSIRMLLTPTHTVHYVWRKFDALMRPFGRGVFPSP 524
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 479 AELFSIRGOTSOGGEPVARPSSIRMLLTPTHTVHYVWRKFDALMRPFGRGVFPSP 538

QY 525 GSPTQES 531
   ||| ||| |||
Db 539 GSPTERS 545

RESULT 12
Q9SQ00 PRELIMINARY; PRT; 552 AA.
AC Q9SQ00;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Putative sodium proton exchanger.
GN F24P17.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
   Rowing C.M., Koo H., Fujii C.Y., Otterback T.R., Barnstead M.E.,
   Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F24P17 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011623; AAF08577.1; .
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR004709; NaH_exchng.
DR InterPro; IPR000676; NaH_exchng.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR PRINTS; PR01084; NAHEXCHNGR.
DR TIGRfams; TIGR00840; b_cpai; 1.
DR PROSITE; PS00453; FKBP_PPASE_1; UNKNOWN_1.
SQ SEQUENCE 552 AA; 61135 MW; FB4317D8A874FCE9 CRC64;

Query Match 70.9%; Score 1931; DB 10; Length 552;
Best Local Similarity 69.6%; Pred. No. 1.7e-134;
Matches 377; Conservative 67; Mismatches 78; Indels 20; Gaps 4;

QY 1 MGMEVAAARLGAALYTTSDYASVSNLFLVALLCACIVLGHLLLEENRWVNESITALI 60
   ||| :||: | :| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 IGLTLMLEKTEALP-ASDHASVSMNLFVALLCACIVLGHLLLEENRWVNESITALI 61

QY 61 TGVVILLMTGKSHLFESEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGT 120
   ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TGVVILLMTGKSHLFESEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGT 121

QY 121 MISFTTISIAAIAIFSRNICTLDVDFLAIGAFSATDSVCTLOVLNQDETPLYSLVF 180
   ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 LISFVLSFGAKHLFEKMNIGDLTIADYLAIGAFSATDSVCTLOVLNQDETPLYSLVF 181

QY 181 GEGVNDATSIVLNALQNFDLVHDAAVLKFGLNFFYFLSLSTFLGVFAGLLSAVLIK 240
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 GEGVNDATSIVLNFAIQRFDLTINSAIALEFAGNFYFLSLSTFLGVFAGLLSAVLIK 241

QY 241 KLYIGRSTDEVALMMLMAYLSYMLAELDLGILTVFFCGIVMSHYTHNVTESRVT 300
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 KLYIGRSTDEVALMMLMAYLSYMLAELDLGILTVFFCGIVMSHYTHNVTESRVT 301

QY 301 TKHATLSFAETFLFYVGMADLDIEKWFASFADRPCKSIGISILLGLVIGRAAPVF 360
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 TKHTFAAMSFLAEIFIFYVGMADLDIEKWDVVRNSPGQSGVSSILLGLLIGRAAPVF 361

QY 361 PLSFLSLNLTKKAPNEKITRQOVVWAGLARGAVSIALAYNKTRSGHTOLHNAIMIT 420
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 PLSFLSLNLTSSPDEKIDKKQVTVWAGLARGAVSIALAYNKTRSGHTOLHNAIMIT 421

QY 421 STITVTLFSTWVFGMTKPLIRLLPASGHPVTS-----EPSSPKSLHSPLITS 469
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 STITVTLFSTWVFGMTKPLIRLLPASGHPVTS-----EPSSPKSLHSPLITS 477

QY 470 MGSQGSLESTTNVVRPSSIRMLLTPTHTVHYVWRKFDALMRPFGRGVFPSPGSTE 529
   ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 QGQSEYDPEQHV----SFRMEFWKSPRAIHVYWRKFDALMRPFGRGVFPSPGSTE 533

QY 530 QS 531
   |
Db 534 NS 535

RESULT 13
Q94BM4 PRELIMINARY; PRT; 546 AA.
AC Q94BM4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Na+/H+ antiporter.
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GN NHX1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triciteae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z., Zhang J., Chen S.;
RT "Isolation and characterization of two Na+/H+ antiporter genes from wheat.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY040245; AAK7673.1; -;
DR InterPro: IPR001179; FKBP_PPase.
DR Pfam: PF00999; Na_H_Exchange; 1.
DR PROSITE: PS00453; FKBP_PPase.1; UNKNOWN.1.
SQ SEQUENCE 546 AA; 59704 MW; 45E1BCAB73E295C6 CRC64;

Query Match 70.6%; Score 1921.5; DB 10; Length 546;
Best Local Similarity 70.0%; Pred. No. 8.6e-134;
Matches 376; Conservative 64; Mismatches 88; Indels 9; Gaps 5;

QY 1 MGEVAAARLGALY- --TSDYASVVSINLFVALLCACIVLGHLLLEENRWYNESITALII 57
Db 1 MGLDGA --LAKYTGAVSDHDSIVAINIFALLCGCIVFGLHLEGNRWYNESITALVL 58

QY 58 GLCTGVILLMTKGSSHLVFSEDLFFIYLLPIIFNAGFOVKKQFFRNPMITILFGA 117
Db 59 GLITGGVILCTKGNSRIILFSEDIFFIYLLPIIFNAGFOVKKQFFRNPMITILFGA 118

QY 118 VCTMSFTTISAAIAIFSRMNICTLDVGDFLAIGAIFSDSVCTLOVNODEPFLYS 177
Db 119 AGTLISFVIITFGAMGLFSKLDVGPLEGLDYLAIGAIFSDSVCTLOVNODEAPLYS 178

QY 178 LVFEGGVNDATSIYLFNALQNFOLVHIDAAVLFKLGNEFFYLSSTFLGFGAGLLSAY 237
Db 179 LVFEGGVNDATSVVLFNAIONIDINHDVFLQFGLKFLYFTSIVLGVAAAGLLSAY 238

QY 238 IIKLYIGRSTDRVALMMLMAYLSYMLAEELDLGSLTVFFFCGIVMSHYTWHNVTESS 297
Db 239 IIKLCFAHSTDRVALMMLMAYLSYMLAEELDLGSLTVFFFCGIVMSHYTWHNVTESS 298

QY 298 RVTKHAFATLSFAETFLYVGMADALIEKWEFASDPKSGISILLGLVLIGRAA 357
Db 299 RVTKHAFATLSFAETFLYVGMADALIDKWLASSPKPKPALSAVILGLVWVGRAA 358

QY 358 FVFPFLSLNLTKKAPNEKITRWQOVVITWAGLMRGAVSIALAYNKFTSGHTOLHGNAI 417
Db 359 FVFPFLSLNLSKKESHPKISFNQOVVITWAGLMRGAVSIALAYNKFTSGHTAVRVNAV 418

QY 418 MITSTIIVLFSTVWFGMTKPLIRLLLPASGHPVTSEPPSKLSHSPLLTSMOGSDLES 477
Db 419 MITSTIIVLFSTVWFGMLTKPLINLIPP --RPGTAADISSQSGLDPLTASLLGSDPFD- 475

QY 478 TTNIVRPSLRMLLTKPTHTVHYVYWRKFDDALMRPMFGGRCGFVFPSPGSPTEQS-HG 533
Db 476 VGQLTPQTNLOLYLLMTFRSHRVWRKFDDKFMRFMGGRCGFVFPVPGSPIERSVHG 532

RESULT 14
Q93YH2
ID Q93YH2 PRELIMINARY; PRT; 534 AA.
AC Q93YH2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Na+/H+ antiporter, isoform 1.
GN NHX1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RA Venema K., Belver A., Donaire J.;
RT "Cloning and characterization of two Na+/H+ antiporter isoforms from tomato.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ306630; CAC84522.1; -;
DR InterPro: IPR000676; NaH_Exchange.
DR Pfam: PF00999; Na_H_Exchange; 1.
SQ SEQUENCE 534 AA; 59037 MW; E4E736FA4A0C0791 CRC64;

Query Match 69.0%; Score 1879; DB 10; Length 534;
Best Local Similarity 68.8%; Pred. No. 1.1e-130;
Matches 369; Conservative 69; Mismatches 90; Indels 8; Gaps 5;

QY 1 MGEVAAARLG-ALYTTSDYASVVSINLFVALLCACIVLGHLLLEENRWYNESITALII 59
Db 1 MGLD- AVALRGVLSLSDGQSVDSITLFAVLLCGCIVLGHLLLEESRWINDSITLVLIGL 59

QY 60 CTGVILLMTKGSSHLVFSEDLFFIYLLPIIFNAGFOVKKQFFRNPMITILFGAVG 119
Db 60 STGGIILITTKGSSHLLEFEQLFFIYVLPPIIFNAGFOVKKQFFRNPMITILFGAVG 119

QY 120 TMISFTTISAAIAIFSRMNICTLDVGDFLAIGAIFSDSVCTLOVNODEPFLYS 179
Db 120 TLISFIIISFGAKELLDIGLELDYLAIGAIFSDSVCTLOVNODEPFLYS 179

QY 180 FEGGVNDATSVVLFNALQNFOLVHIDAAVLFKLGNEFFYLSSTFLGFGAGLLSAY 239
Db 180 FEGGVNDATSVVLFNAIONIDINHDVFLQFGLKFLYFTSIVLGVAAAGLLSAY 239

QY 240 KLYIGRSTDRVALMMLMAYLSYMLAEELDLGSLTVFFFCGIVMSHYTWHNVTESS 299
Db 240 KLYIGRSTDRVALMMLMAYLSYMLAEELDLGSLTVFFFCGIVMSHYTWHNVTESS 299

QY 300 TTGHAFATLSFAETFLYVGMADALIEKWEFASDPKSGISILLGLVLIGRAAFV 359
Db 300 TTGHAFATLSFAETFLYVGMADALIEKWEFASDPKSGISILLGLVLIGRAAFV 359

QY 360 PFLSFLSLNLTKKAPNEKITRWQOVVITWAGLMRGAVSIALAYNKFTSGHTOLHGNAI 419
Db 360 PFLSFLSCLARSHDKFLQVITWAGLMRGAVSIALAYNKFTSGHTOLHGNAI 419

QY 420 TSTIIVLFSTVWFGMTKPLIRLLLPASGHPVTSEPPSKLSHSPLLTSMOGSDLE-ST 478
Db 420 TSTIIVLFSTVWFGMLTKPLIRLLLPSS-QGFNNLISSEQSFARPLITNEQELEMG 478

QY 479 TTNIVRPSLRMLLTKPTHTVHYVYWRKFDDALMRPMFGGRCGFVFPSPGSPTEQSHG 534
Db 479 VDPVRPSGLSILLKEPSYTIHWHRRFDDAFMRPLFGGRCGFVDPAP----ELSKGG 530

RESULT 15
O04655
ID O04655 PRELIMINARY; PRT; 457 AA.
AC O04655;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE A_TM021B04.4 protein.
GN A_TM021B04.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Dante M., Wamsley P., Gibson A.;
RT "The sequence of A. thaliana TM021B04.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Wash-U;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Waterston R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF007271; AAB61069.1; -.
DR InterPro; IPR001179; FKBP_PPase.
DR InterPro; IPR000676; Nah_Exchange.
DR Pfam; PF00999; Nah_Exchange; 1.
DR PROSITE; PS00453; FKBP_PPase_1; UNKNOWN_1.
SQ SEQUENCE 457 AA; 50611 MW; 0AF2F235F1A258EE CRC64;

Query Match 62.4%; Score 1698.5; DB 10; Length 457;
Best Local Similarity 74.0%; Pred. No. 2e-117;
Matches 333; Conservative 45; Mismatches 51; Indels 21; Gaps 3;

QY 3 MEVAARLGALYTTSDYASVSWINLFAVALLCACIVLGHLLLENRWNNESITALLIGLCTG 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 LDSLVSKLPSL-STSDHASVVALNLFVALLCACIVLGHLLLENRWNNESITALLIGLCTG 60
QY 63 VVILLMTKCKSHLFESEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGTMI 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 VTILLISKGKSHLFESEDLFFIYLLPPIIFNAGFQVKKKOFFRNFMTITLFGAVGTII 120
QY 123 SPTTISIAAIAIFSRMNIQTLDVGDFLAIGAIFSATDSVCTLQVLNQDETFFLYSLVFE 182
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 SCTIISLGVTQFFKKLDICTFDLGDYLAIGAIFAATDSVCTLQVLNQDETFFLYSLVFE 180
QY 183 GYVNDATSIIVLFNALQNFEDLVHIDAADVVLKFLGNFFYFLSSTFLGV-----F 230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 GYVNDATSVVFNAIQSEFDLTHLNHEAAFHLLGNFLYLLSTLLGAASVPLFSSLPFFL 240
QY 231 AGLSAYIICKLYIG-----RHSTDREVALMMAYLSYMLAELDLGILTVFFCG 282
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 TGLISAYVIKKLYFGRWPHINCHRHSTDREVALMMAYLSYMLAELDLGILTVFFCG 300
QY 283 IVMSHYTHNVTESSRVTTKHAFTLSFIAETFFLYVGMADALDIEKWEFASDRPGKSIG 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 IVMSHYTHNVTESSRIITTKHTFATLSFLAETFFLYVGMADALDIDKRSVSDTPTGTSIA 360
QY 343 ISSILGLVLIGRAAFVPLFSLNLTKKAPNEKITWRQOVVWAGLMRGAVSTALAYN 402
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 VSSILMGLVMVGRAAFVPLFSLNLAQKKNQSEKINFNQVVIWWSGLMRGAVSMALAYN 420
QY 403 KFRSGHTOLHGNAIMTSTITVFLFSTMV 432
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 KFRAGHTDVRGNAIMTSTITVCLFSIVV 450

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Search completed: March 26, 2003, 18:53:48
Job time : 41 secs

